GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 23.9545 Seconds
(without alignments)
85.823 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	100.0	31	3	US-09-070-504-23	Sequence 23, Appl
2	163	100.0	31	3	US-09-011-922A-3	Sequence 3, Appli
3	163	100.0	31	3	US-09-011-922A-14	Sequence 14, Appl
4	163	100.0	31	4	US-09-280-501-9	Sequence 9, Appli
5	163	100.0	31	4	US-09-813-345C-23	Sequence 23, Appl
6	163	100.0	38	4	US-09-280-501-6	Sequence 6, Appli
7	163	100.0	40	4	US-09-280-501-11	Sequence 11, Appl
8	163	100.0	52	3	US-09-070-504-14	Sequence 14, Appl
9	163	100.0	52	4	US-09-813-345C-14	Sequence 14, Appl
10	163	100.0	185	1	US-08-233-389C-1	Sequence 1, Appli
11	163	100.0	185	2	US-08-801-863-1	Sequence 1, Appli
12	163	100.0	185	2	US-08-486-596A-1	Sequence 1, Appli
13	163	100.0	185	2	US-09-004-713-1	Sequence 1, Appli
14	158	96.9	30	4	US-09-280-501-5	Sequence 5, Appli
15	157	96.3	188	1	US-08-233-389C-3	Sequence 3, Appli
16	157	96.3	188	2	US-08-801-863-3	Sequence 3, Appli
17	157	96.3	188	2	US-08-486-596A-3	Sequence 3, Appli
18	157	96.3	188	2	US-09-004-713-3	Sequence 3, Appli
19	154	94.5	29	4	US-09-280-501-4	Sequence 4, Appli
20	150	92.0	40	4	US-09-280-501-8	Sequence 8, Appli
21	150	92.0	50	4	US-09-280-501-7	Sequence 7, Appli
22	149	91.4	28	4	US-09-280-501-3	Sequence 3, Appli
23	148	90.8	50	3	US-09-070-504-15	Sequence 15, Appl
24	148	90.8	50	4	US-09-813-345C-15	Sequence 15, Appl
25	144	88.3	27	4	US-09-280-501-2	Sequence 2, Appli
26	140	85.9	26	4	US-09-280-501-1	Sequence 1, Appli
27	123	75.5	23	4	US-09-280-501-17	Sequence 17, Appl
28	112	68.7	21	4	US-09-280-501-16	Sequence 16, Appl
29	74	45.4	13	4	US-09-280-501-15	Sequence 15, Appl
30	68	41.7	13	4	US-09-280-501-10	Sequence 10, Appl
31	57	35.0	13	3	US-09-011-922A-2	Sequence 2, Appli
32	52	31.9	775	2	US-08-966-388-4	Sequence 4, Appli
33	52	31.9	775	3	US-09-188-403-4	Sequence 4, Appli
34	52	31.9	775	3	US-09-188-404-4	Sequence 4, Appli
35	52	31.9	775	3	US-09-281-259-4	Sequence 4, Appli
36	52	31.9	1005	4	US-09-252-991A-24655	Sequence 24655, A
37	51	31.3	10	2	US-08-934-222-17	Sequence 17, Appl
38	51	31.3	10	2	US-08-933-402-17	Sequence 17, Appl
39	51	31.3	10	2	US-09-207-621-17	Sequence 17, Appl
40	51	31.3	10	2	US-08-532-818-17	Sequence 17, Appl
41	51	31.3	10	3	US-09-231-797-17	Sequence 17, Appl
42	51	31.3	10	3	US-08-934-224-17	Sequence 17, Appl
43	51	31.3	10	3	US-08-933-843-17	Sequence 17, Appl
44	51	31.3	10	3	US-08-934-223-17	Sequence 17, Appl
45	51	31.3	10	3	US-09-413-492-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 100.0%; Score 163; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
||||||||||||||||||||||||||||||
Db 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

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RESULT 2
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
;  GENERAL INFORMATION:
;    APPLICANT:  Cuttitta, Frank; Martinez,
;    APPLICANT:  Alfredo; Miller, Mae Jean; Unsworth, Edward
;    APPLICANT:  J.; Hook, William; Walsh, Thomas; Grey,
;    APPLICANT:  Karen; Macri, Charles
;    TITLE OF INVENTION:  Functional Role of
;    TITLE OF INVENTION:  Adrenomedullin (AM) and the Gene-Related
;    TITLE OF INVENTION:  Product (PAMP) in Human Pathology and
;    TITLE OF INVENTION:  Physiology
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS WORD 97
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,922A
;      FILING DATE:  17-Feb-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,514
;      FILING DATE:  18-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,936
;      FILING DATE:  30-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/013,172
;      FILING DATE:  12-Mar-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/13286
;      FILING DATE:  16-Aug-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leslie A. Serunian
;      REGISTRATION NUMBER:  35,353
;      REFERENCE/DOCKET NUMBER:  2026-4202US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      NAME/KEY:  P072
;      OTHER INFORMATION:  PreproAM(116-146)
US-09-011-922A-3

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 3
US-09-011-922A-14
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; Sequence 14, Application US/09011922A
; Patent No. 6320022
;  GENERAL INFORMATION:
;    APPLICANT:  Cuttitta, Frank; Martinez,
;    APPLICANT:  Alfredo; Miller, Mae Jean; Unsworth, Edward
;    APPLICANT:  J.; Hook, William; Walsh, Thomas; Grey,
;    APPLICANT:  Karen; Macri, Charles
;    TITLE OF INVENTION:  Functional Role of
;    TITLE OF INVENTION:  Adrenomedullin (AM) and the Gene-Related
;    TITLE OF INVENTION:  Product (PAMP) in Human Pathology and
;    TITLE OF INVENTION:  Physiology
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS WORD 97
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,922A
;      FILING DATE:  17-Feb-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,514
;      FILING DATE:  18-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,936
;      FILING DATE:  30-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/013,172
;      FILING DATE:  12-Mar-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/13286
;      FILING DATE:  16-Aug-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leslie A. Serunian
;      REGISTRATION NUMBER:  35,353
;      REFERENCE/DOCKET NUMBER:  2026-4202US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      OTHER INFORMATION:  Synthetic homolog of
;      OTHER INFORMATION:  two-thirds of the intact AM peptide
US-09-011-922A-14

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 4
US-09-280-501-9
; Sequence 9, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
```

```
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-9

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 5
US-09-813-345C-23
; Sequence 23, Application US/09813345C
; Patent No. 6756205
; GENERAL INFORMATION:
;  APPLICANT: CREIGHTON UNIVERSITY
;  APPLICANT:  SMITH, Derek D.
;  APPLICANT:  SAHA, Shankar
;  APPLICANT:  ABEL, Peter W.
;  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 180.00020102
;  CURRENT APPLICATION NUMBER: US/09/813,345C
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: 09/070,504
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-09-813-345C-23

  Query Match             100.0%;  Score 163;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 6
US-09-280-501-6
; Sequence 6, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-6

  Query Match             100.0%;  Score 163;  DB 4;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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Db          8 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 38


RESULT 7
US-09-280-501-11
; Sequence 11, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-11

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  Best Local Similarity   100.0%;  Pred. No. 4.9e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         10 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 40


RESULT 8
US-09-070-504-14
; Sequence 14, Application US/09070504
; Patent No. 6268474
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Derek D.
;    APPLICANT:  Saha, Shankar
;    APPLICANT:  Abel, Peter W.
;    TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;    TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;      STREET:  119 No. 6268474th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/070,504
;       FILING DATE:  30-APR-1998
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McCormack, Myra H
;       REGISTRATION NUMBER:  36,602
;       REFERENCE/DOCKET NUMBER:  180.00020101
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612/305-1220
;       TELEFAX:  612/305-1228
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  52 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-070-504-14

  Query Match             100.0%;  Score 163;  DB 3;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 9
US-09-813-345C-14
; Sequence 14, Application US/09813345C
; Patent No. 6756205
; GENERAL INFORMATION:
;  APPLICANT: CREIGHTON UNIVERSITY
;  APPLICANT:  SMITH, Derek D.
;  APPLICANT:  SAHA, Shankar
;  APPLICANT:  ABEL, Peter W.
;  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 180.00020102
;  CURRENT APPLICATION NUMBER: US/09/813,345C
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: 09/070,504
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-09-813-345C-14

  Query Match             100.0%;  Score 163;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 10
US-08-233-389C-1
; Sequence 1, Application US/08233389C
; Patent No. 5639855
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,389C
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-233-389C-1

  Query Match             100.0%;  Score 163;  DB 1;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 11
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,863
;      FILING DATE:  CONCURRENTLY HEREWITH
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
```

```
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  SHGN-5 DIV3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 596-9000
;       TELEFAX:  (212) 596-9090
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  185 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-801-863-1

  Query Match             100.0%;  Score 163;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 12
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,596A
;      FILING DATE:  JUNE 7, 1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-486-596A-1

  Query Match             100.0%;  Score 163;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 13
US-09-004-713-1
; Sequence 1, Application US/09004713
; Patent No. 5910416
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/004,713
;      FILING DATE:  JANUARY 7, 1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5 DIV2 CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-004-713-1

  Query Match             100.0%;  Score 163;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 14
US-09-280-501-5
; Sequence 5, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-5
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  Query Match             96.9%;  Score 158;  DB 4;  Length 30;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||||||||||||||||||||||||||||||
Db          1 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 30


RESULT 15
US-08-233-389C-3
; Sequence 3, Application US/08233389C
; Patent No. 5639855
;  GENERAL INFORMATION:
;    APPLICANT:  KITAMURA, Kazuo
;    APPLICANT:  KANGAWA, Kenji
;    APPLICANT:  MATSUO, Hisayuki
;    APPLICANT:  ETO, Tanenao
;    TITLE OF INVENTION:  ADRENOMEDULLIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/233,389C
;      FILING DATE:  26-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HALEY Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  SHGN-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  188 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-233-389C-3

  Query Match             96.3%;  Score 157;  DB 1;  Length 188;
  Best Local Similarity   96.8%;  Pred. No. 3e-17;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||| ||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


Search completed: January  5, 2005, 08:45:19
Job time : 24.9545 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:23 ; Search time 67.0682 Seconds
(without alignments)
69.533 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76	100.0	13	2	AAW25159	Aaw25159 Human pre
2	57	75.0	26	7	ADF16710	Adf16710 Human alb
3	57	75.0	27	8	ADP18404	Adp18404 Neurogene
4	57	75.0	31	2	AAW25160	Aaw25160 Human pre
5	57	75.0	31	4	AAB91762	Aab91762 Adrenomed
6	57	75.0	31	4	AAE09827	Aae09827 Human adr
7	57	75.0	31	7	ADC25153	Adc25153 Human ang
8	57	75.0	31	8	ADP18403	Adp18403 Neurogene
9	57	75.0	40	4	AAB91768	Aab91768 Adrenomed
10	57	75.0	50	4	AAE09819	Aae09819 Rat adren
11	57	75.0	50	7	ADE51616	Ade51616 Adrenomed
12	57	75.0	52	4	AAB91765	Aab91765 Adrenomed
13	57	75.0	52	4	AAB91759	Aab91759 Adrenomed
14	57	75.0	52	4	AAB75110	Aab75110 Human adr
15	57	75.0	52	4	AAE09818	Aae09818 Human adr
16	57	75.0	52	6	ABP55104	Abp55104 Human adr
17	57	75.0	52	7	ADC25152	Adc25152 Human ang
18	57	75.0	52	7	ADG91993	Adg91993 Human mat
19	57	75.0	52	8	ADL91994	Adl91994 Adrenomed
20	57	75.0	52	8	ADM94034	Adm94034 Human AM
21	57	75.0	52	8	ADN03278	Adn03278 Exemplary
22	57	75.0	52	8	ADM98309	Adm98309 Mature hu
23	57	75.0	52	8	ADP18429	Adp18429 Neurogene
24	57	75.0	52	8	ADP18402	Adp18402 Neurogene
25	57	75.0	53	4	AAB75111	Aab75111 Glycine e
26	57	75.0	53	4	AAB75112	Aab75112 Glycine e
27	57	75.0	53	6	ABJ18665	Abj18665 Universal
28	57	75.0	62	4	AAB75113	Aab75113 Linker pe
29	57	75.0	91	8	ADF55556	Adf55556 Active hu
30	57	75.0	120	4	AAB75123	Aab75123 UspA(1-56
31	57	75.0	120	4	AAB75122	Aab75122 UspA(1-57
32	57	75.0	120	6	ABJ18669	Abj18669 Universal
33	57	75.0	120	6	ABJ18670	Abj18670 Universal
34	57	75.0	147	4	AAB75124	Aab75124 UspA(1-84
35	57	75.0	147	6	ABJ18671	Abj18671 Universal
36	57	75.0	170	4	AAB75114	Aab75114 Thioredox
37	57	75.0	185	4	AAB60344	Aab60344 Human adr
38	57	75.0	185	4	AAB60346	Aab60346 Rat adren
39	57	75.0	185	4	AAB49697	Aab49697 Human adr
40	57	75.0	185	4	AAB49699	Aab49699 Rat adren
41	57	75.0	185	6	ABP72347	Abp72347 Adrenomed
42	57	75.0	185	7	ADA27595	Ada27595 Human adr
43	57	75.0	185	8	ADF55557	Adf55557 Human adr
44	57	75.0	185	8	ADN10849	Adn10849 Human adr
45	57	75.0	185	8	ADM98308	Adm98308 Human pre

ALIGNMENTS

RESULT 1
AAW25159
ID AAW25159 standard; peptide; 13 AA.
XX
AC AAW25159;
XX
DT 08-DEC-1997 (first entry)
XX
DE Human preproadrenomedullin derived immunogen, PO71.
XX
KW Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
KW skin; blood related; disease; type II diabetes; preeclampsia;
KW neurotransmission regulation; allergy; mast cell degranulation;
KW antibacterial; antifungal; wound repair.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .13
FT /note= "residues 122-131 of preproadrenomedullin with Tyr
FT -Gly-Gly attached at N-terminus"
FT Modified-site 13
FT /note= "amidated"
XX
PN WO9707214-A1.
XX
PD 27-FEB-1997.
XX
PF 16-AUG-1996; 96WO-US013286.
XX
PR 18-AUG-1995; 95US-0002514P.
PR 30-AUG-1995; 95US-0002936P.
PR 12-MAR-1996; 96US-0013172P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cuttitta F, Martinez A, Miller MJ, Unsworth EJ, Hook W, Walsh T;
PI Gray K, Macri C;
XX
DR WPI; 1997-165298/15.
XX
PT Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used in
PT the diagnosis and treatment of type II diabetes and cancer.
XX
PS Claim 1; Page 43; 106pp; English.
XX
CC Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20 were used
CC for the production of anti-AM antibodies (Ab). PO70 represents preproAM

```
CC   amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at the N-
CC   terminus, PO71 represents preproAM aa 122-131 with the sequence Tyr-Gly-
CC   Gly attached at the N-terminus, PO72 represents preproAM aa 116-146 and
CC   PAMP-20 represents the proAM N-terminus. The Ab are useful for the
CC   prevention and/or treatment of cancers, e.g. adrenal, nervous system,
CC   lung, colon, ovarian and breast cancer by inhibiting cell growth. They
CC   are also useful for regulating insulin secretion and blood glucose
CC   metabolism and therefore for treating and/or preventing diabetes type II.
CC   They may be used for the diagnosis or treatment of conditions relating to
CC   pregnancy e.g. preeclampsia. The Ab are also useful for the following:
CC   (i) regulating neurotransmission or neuron growth in areas of the central
CC   nervous system; (ii) lessening or inhibiting mast cell degranulation and
CC   hence reducing the effects of an allergic response; (iii) inhibiting or
CC   preventing bacterial and fungal growth (to treat infection); (iv)
CC   facilitating wound healing; and (v) promoting organ and bone development
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 76;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGGHQIYQFTDKD 13
              |||||||||||||
Db          1 YGGHQIYQFTDKD 13


RESULT 2
ADF16710
ID   ADF16710 standard; protein; 26 AA.
XX
AC   ADF16710;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human albumin fusion protein-related protein SeqID1812.
XX
KW   albumin fusion protein; albumin activity; human serum albumin;
KW   serum osmotic pressure; shelf-life; stability; antidiabetic;
KW   gene therapy; diabetes mellitus; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003060071-A2.
XX
PD   24-JUL-2003.
XX
PF   23-DEC-2002; 2002WO-US040891.
XX
PR   21-DEC-2001; 2001US-0341811P.
PR   24-JAN-2002; 2002US-0350358P.
PR   28-JAN-2002; 2002US-0351360P.
PR   26-FEB-2002; 2002US-0359370P.
PR   28-FEB-2002; 2002US-0360000P.
PR   27-MAR-2002; 2002US-0367500P.
PR   08-APR-2002; 2002US-0370227P.
PR   10-MAY-2002; 2002US-0378950P.
PR   24-MAY-2002; 2002US-0382617P.
PR   28-MAY-2002; 2002US-0383123P.
PR   05-JUN-2002; 2002US-0385708P.
PR   10-JUL-2002; 2002US-0394625P.
PR   24-JUL-2002; 2002US-0398008P.
PR   09-AUG-2002; 2002US-0402131P.
PR   13-AUG-2002; 2002US-0402708P.
PR   18-SEP-2002; 2002US-0411355P.
PR   18-SEP-2002; 2002US-0411426P.
PR   02-OCT-2002; 2002US-0414984P.
PR   11-OCT-2002; 2002US-0417611P.
PR   23-OCT-2002; 2002US-0420246P.
PR   05-NOV-2002; 2002US-0423623P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA   (PRIN-) PRINCIPIA PHARM CORP.
XX
PI   Ballance DJ,  Turner AJ,  Rosen CA,  Haseltine WA;
XX
DR   WPI; 2003-598517/56.
DR   N-PSDB; ADF16384.
XX
PT   New albumin fusion protein, useful for preparing a composition for
PT   treating diabetes mellitus.
XX
PS   Example 4; SEQ ID NO 1812; 24pp; English.
XX
CC   This invention relates to a novel albumin fusion protein having albumin
CC   or biological activity. Human serum albumin is responsible for a
CC   significant proportion of the osmotic pressure of serum and also
CC   functions as a carrier of endogenous and exogenous ligands. The fusion of
CC   albumin to a therapeutic protein may increase shelf-life and stability of
CC   the therapeutic protein. The albumin fusion protein of the invention may
CC   allow production of compositions with antidiabetic activity whilst the
CC   nucleotide sequence which encodes it may be useful for gene therapy. The
CC   albumin fusion protein is useful for preparing a composition for treating
CC   diabetes mellitus. The present sequence is that of a therapeutic protein
CC   which was fused with human albumin to create a novel albumin fusion
CC   protein of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ   Sequence 26 AA;

  Query Match             75.0%;  Score 57;  DB 7;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          2 HQIYQFTDKD 11


RESULT 3
ADP18404
ID   ADP18404 standard; peptide; 27 AA.
XX
AC   ADP18404;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Neurogenesis modulation-related peptide SeqID18.
XX
KW   neurogenesis modulation; neural tissue; central nervous system disorder;
KW   neurodegenerative; ischaemic; learning and memory disorder;
KW   neurological trauma; nootropic; neuroprotective; CNS-Gen;
KW   cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;
KW   haemostatic; hypertensive; muscular-Gen; ophthalmological;
KW   antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;
KW   neural stem cell; progenitor cell;
KW   neural tissue G-protein coupled receptor activator; neurogenesis inducer;
KW   intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;
KW   intracellular neural Ca 2+ enhancer; Parkinson's disease;
KW   Parkinson's disorder; Huntington's disease; Alzheimer's disease;
KW   multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;
KW   progressive supranuclear palsy; Lewy body disease; spinal ischaemia;
KW   ischaemic stroke; cerebral infarction; spinal cord injury;
KW   cancer-related brain; spinal cord injury; multi-infarct dementia;
KW   geriatric dementia; cAMP level; embryonic tissue; human.
XX
OS   Homo sapiens.
XX
PN   WO2004045592-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-IB005311.
XX
```

PR 20-NOV-2002; 2002US-0427912P.
XX
PA (NEUR-) NEURONOVA AB.
PA (BERT/) BERTILSSON G.
PA (ERLA/) ERLANDSSON R.
PA (FRIS/) FRISEN J.
PA (HAEG/) HAEGESTRAND A.
PA (HEID/) HEIDRICH J.
PA (HELL/) HELLSTROEM K.
PA (HAEG/) HAEGGBLAD J.
PA (JANS/) JANSSON K.
PA (KORT/) KORTESMAA J.
PA (LIND/) LINDQUIST P.
PA (LUND/) LUNDH H.
PA (MCGU/) MCGUIRE J.
PA (MERC/) MERCER A.
PA (NJBE/) NJBERG K.
PA (OSSO/) OSSOINAK A.
PA (PATR/) PATRONE C.
PA (ROEN/) ROENNHOLM H.
PA (ZACH/) ZACHRISSON O.
PA (WIKS/) WIKSTROEM L.
XX
PI Bertilsson G, Erlandsson R, Frisen J, Haegestrand A, Heidrich J;
PI Hellstroem K, Haeggblad J, Jansson K, Kortesmaa J, Lindquist P;
PI Lundh H, Mcguire J, Mercer A, Njberg K, Ossoinak A, Patrone C;
PI Roennholm H, Zachrisson O, Wikstroem L;
XX
DR WPI; 2004-449666/42.
XX
PT Use of agent(s) that elevate intracellular cyclic adenosine monophosphate
PT or intracellular calcium levels in neural tissue for modulating
PT neurogenesis to treat central nervous system disorder.
XX
PS Disclosure; SEQ ID NO 18; 77pp; English.
XX
CC This invention relates to a novel method of modulating neurogenesis in
CC the neural tissue of a patient exhibiting symptom(s) of a central nervous
CC system disorder, such as neurodegenerative, ischaemic or learning and
CC memory disorder or neurological trauma. The method involves at least one
CC agent (A) that elevates intracellular cyclic adenosine monophosphate
CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+
CC levels in the neural tissue, which is administered where (A) modulates
CC and (B) induces neurogenesis. The invention may be useful for the
CC production of compounds with a nootropic, neuroprotective, CNS-Gen,
CC cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian.
CC haemostatic, hypertensive, muscular-Gen, ophthalmological,
CC antiinflammatory, analgesic or antidiabetic activity. These compounds may
CC act as neurogenesis modulators, neural stem or progenitor cell
CC proliferation, differentiation and/or migration modulators, neural tissue
CC G-protein coupled receptor activators, neurogenesis inducers,
CC intracellular neural cAMP enhancers, intracellular neural cAMP
CC stimulators or intracellular neural Ca 2+ enhancers. The invention is
CC useful for modulating neurogenesis in neural tissue of a patient
CC exhibiting at least one symptom of central nervous system disorder, such
CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,
CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,
CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,
CC spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord
CC injury, cancer-related brain and spinal cord injury, multi-infarct
CC dementia and geriatric dementia; for increasing the intracellular levels
CC of or stimulating cAMP levels in a cell (preferably a cell from a neural
CC tissue); and for in vitro modulation of neurogenesis. The agent modulates
CC neurogenesis in neural tissue by modulating proliferation,
CC differentiation, migration or survival of neural stem cells or progenitor
CC cells in the tissue; by maintaining or increasing the amount or
CC percentage of doublecortin positive cells in the neural tissue relative
CC to a patient not dosed with the agent or by activation of a G-protein
CC coupled receptor in the neural tissue. The method results in elevation of
CC cAMP levels of the neural stem cells by over 20% compared to untreated
CC tissue. The in vivo induction of neurogenesis allows treatment of
CC disorders caused by cell loss, injury or disease by endogenous
CC replacement and obviates the need for transplanting foreign cells into a
CC patient. Neurogenesis can also be induced by administration of the
CC neurogenesis-modulating agent directly into a desired site, which avoids
CC unnecessary systemic administration and possible side effects and further
CC provides an alternative to the use of drugs and the controversial use of
CC large quantities of embryonic tissue for treatment of Parkinson's
CC disease. The present sequence is that of a polypeptide which has been
CC shown to have the ability to increase intracellular cAMP levels and which
CC is related to the method of the invention.
XX
SQ Sequence 27 AA;

Query Match 75.0%; Score 57; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 3 HQIYQFTDKD 12

RESULT 4
AAW25160
ID AAW25160 standard; peptide; 31 AA.
XX
AC AAW25160;
XX
DT 08-DEC-1997 (first entry)
XX
DE Human preproadrenomedullin derived immunogen, PO72.
XX
KW Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
KW skin; blood related; disease; type II diabetes; preeclampsia;
KW neurotransmission regulation; allergy; mast cell degranulation;
KW antibacterial; antifungal; wound repair.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .31
FT /note= "residues 116-146 of preproadrenomedullin"
FT Modified-site 31
FT /note= "amidated"
XX
PN WO9707214-A1.
XX
PD 27-FEB-1997.
XX
PF 16-AUG-1996; 96WO-US013286.
XX
PR 18-AUG-1995; 95US-0002514P.
PR 30-AUG-1995; 95US-0002936P.
PR 12-MAR-1996; 96US-0013172P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cuttitta F, Martinez A, Miller MJ, Unsworth EJ, Hook W, Walsh T;
PI Gray K, Macri C;
XX
DR WPI; 1997-165298/15.
XX
PT Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used in
PT the diagnosis and treatment of type II diabetes and cancer.
XX
PS Claim 1; Page 43; 106pp; English.
XX
CC Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20 were used
CC for the production of anti-AM antibodies (Ab). PO70 represents preproAM
CC amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at the N-
CC terminus, PO71 represents preproAM aa 122-131 with the sequence Tyr-Gly-
CC Gly attached at the N-terminus, PO72 represents preproAM aa 116-146 and
CC PAMP-20 represents the proAM N-terminus. The Ab are useful for the
CC prevention and/or treatment of cancers, e.g. adrenal, nervous system,
CC lung, colon, ovarian and breast cancer by inhibiting cell growth. They

```
CC   are also useful for regulating insulin secretion and blood glucose
CC   metabolism and therefore for treating and/or preventing diabetes type II.
CC   They may be used for the diagnosis or treatment of conditions relating to
CC   pregnancy e.g. preeclampsia. The Ab are also useful for the following:
CC   (i) regulating neurotransmission or neuron growth in areas of the central
CC   nervous system; (ii) lessening or inhibiting mast cell degranulation and
CC   hence reducing the effects of an allergic response; (iii) inhibiting or
CC   preventing bacterial and fungal growth (to treat infection); (iv)
CC   facilitating wound healing; and (v) promoting organ and bone development
XX
SQ   Sequence 31 AA;

  Query Match             75.0%;  Score 57;  DB 2;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 5
AAB91762
ID   AAB91762 standard; peptide; 31 AA.
XX
AC   AAB91762;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:938.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US013576.
XX
PR   17-MAY-1999;   99US-0134406P.
PR   10-SEP-1999;   99US-0153406P.
PR   15-OCT-1999;   99US-0159783P.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity.
XX
PS   Disclosure; Page 499-500; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity in
CC   vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention
XX
SQ   Sequence 31 AA;

  Query Match             75.0%;  Score 57;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 6
AAE09827
ID   AAE09827 standard; peptide; 31 AA.
XX
AC   AAE09827;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Human adrenomedullin peptide #2.
XX
KW   Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW   CGRP-receptor identification; adrenomedullin.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   31
FT                   /note= "C-terminal amide"
XX
PN   US6268474-B1.
XX
PD   31-JUL-2001.
XX
PF   30-APR-1998;   98US-00070504.
XX
PR   30-APR-1998;   98US-00070504.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Smith DD,  Saha S,  Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT   receptor activity.
XX
PS   Claim 5; Col 6; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide calcitonin
CC   gene related peptide (CGRP) and other members of the CGRP superfamily.
CC   The invention also relates to amino the terminal modifications of
CC   peptides to improve their ability to bind to a member of the CGRP-
CC   receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC   activity which can be used in vitro e.g. in assays to identify and/or
CC   isolate CGRP receptors or with intact cells either in vitro or in vivo to
CC   inhibit the effect of CGRP binding to its receptor. The present sequence
CC   is human adrenomedullin peptide
XX
SQ   Sequence 31 AA;

  Query Match             75.0%;  Score 57;  DB 4;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16
```

RESULT 7
ADC25153
ID ADC25153 standard; peptide; 31 AA.
XX
AC ADC25153;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human angiogenesis inhibiting peptide #SEQ ID 2.
XX
KW Cytostatic; gene therapy; cancer; stomach; colon; pulmonary; ovarian;
KW liver; pancreatic; human.
XX
OS Homo sapiens.
XX
PN WO2003078460-A1.
XX
PD 25-SEP-2003.
XX
PF 19-MAR-2003; 2003WO-JP003344.
XX
PR 19-MAR-2002; 2002JP-00075575.
XX
PA (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE CO.
XX
PI Kobayashi M;
XX
DR WPI; 2003-767505/72.
XX
PT Peptides with effect on inhibiting angiogenesis in cancer cells and
PT inhibiting proliferation of cancer cells, and encoded polynucleotides,
PT applicable in drug compositions for treating cancer.
XX
PS Example 2; SEQ ID NO 2; 41pp; Japanese.
XX
CC The invention relates to peptides comprising an amino acid sequence
CC derived from a fully defined 52 amino acid sequence (S1) given in the
CC specification. Peptides may be created by deletion of some amino acids
CC from the N-terminal of S1. The peptides are applicable in drug
CC compositions for treating cancer e.g. stomach cancer, colon cancer,
CC pulmonary cancer, ovarian cancer, liver cancer or pancreatic cancer. The
CC current sequence represents an angiogenesis inhibiting peptide of the
CC invention.
XX
SQ Sequence 31 AA;

Query Match 75.0%; Score 57; DB 7; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 7 HQIYQFTDKD 16

RESULT 8
ADP18403
ID ADP18403 standard; peptide; 31 AA.
XX
AC ADP18403;
XX
DT 26-AUG-2004 (first entry)
XX
DE Neurogenesis modulation-related peptide SeqID17.
XX
KW neurogenesis modulation; neural tissue; central nervous system disorder;
KW neurodegenerative; ischaemic; learning and memory disorder;
KW neurological trauma; nootropic; neuroprotective; CNS-Gen;
KW cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;
KW haemostatic; hypertensive; muscular-Gen; ophthalmological;
KW antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;
KW neural stem cell; progenitor cell;
KW neural tissue G-protein coupled receptor activator; neurogenesis inducer;
KW intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;
KW intracellular neural Ca 2+ enhancer; Parkinson's disease;
KW Parkinson's disorder; Huntington's disease; Alzheimer's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;
KW progressive supranuclear palsy; Lewy body disease; spinal ischaemia;
KW ischaemic stroke; cerebral infarction; spinal cord injury;
KW cancer-related brain; spinal cord injury; multi-infarct dementia;
KW geriatric dementia; cAMP level; embryonic tissue; human.
XX
OS Homo sapiens.
XX
PN WO2004045592-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-IB005311.
XX
PR 20-NOV-2002; 2002US-0427912P.
XX
PA (NEUR-) NEURONOVA AB.
PA (BERT/) BERTILSSON G.
PA (ERLA/) ERLANDSSON R.
PA (FRIS/) FRISEN J.
PA (HAEG/) HAEGESTRAND A.
PA (HEID/) HEIDRICH J.
PA (HELL/) HELLSTROEM K.
PA (HAEG/) HAEGGBLAD J.
PA (JANS/) JANSSON K.
PA (KORT/) KORTESMAA J.
PA (LIND/) LINDQUIST P.
PA (LUND/) LUNDH H.
PA (MCGU/) MCGUIRE J.
PA (MERC/) MERCER A.
PA (NJBE/) NJBERG K.
PA (OSSO/) OSSOINAK A.
PA (PATR/) PATRONE C.
PA (ROEN/) ROENNHOLM H.
PA (ZACH/) ZACHRISSON O.
PA (WIKS/) WIKSTROEM L.
XX
PI Bertilsson G, Erlandsson R, Frisen J, Haegestrand A, Heidrich J;
PI Hellstroem K, Haeggblad J, Jansson K, Kortesmaa J, Lindquist P;
PI Lundh H, Mcguire J, Mercer A, Njberg K, Ossoinak A, Patrone C;
PI Roennholm H, Zachrisson O, Wikstroem L;
XX
DR WPI; 2004-449666/42.
XX
PT Use of agent(s) that elevate intracellular cyclic adenosine monophosphate
PT or intracellular calcium levels in neural tissue for modulating
PT neurogenesis to treat central nervous system disorder.
XX
PS Disclosure; SEQ ID NO 17; 77pp; English.
XX
CC This invention relates to a novel method of modulating neurogenesis in
CC the neural tissue of a patient exhibiting symptom(s) of a central nervous
CC system disorder, such as neurodegenerative, ischaemic or learning and
CC memory disorder or neurological trauma. The method involves at least one
CC agent (A) that elevates intracellular cyclic adenosine monophosphate
CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+
CC levels in the neural tissue, which is administered where (A) modulates
CC and (B) induces neurogenesis. The invention may be useful for the
CC production of compounds with a nootropic, neuroprotective, CNS-Gen,
CC cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian.
CC haemostatic, hypertensive, muscular-Gen, ophthalmological,
CC antiinflammatory, analgesic or antidiabetic activity. These compounds may
CC act as neurogenesis modulators, neural stem or progenitor cell
CC proliferation, differentiation and/or migration modulators, neural tissue
CC G-protein coupled receptor activators, neurogenesis inducers,
CC intracellular neural cAMP enhancers, intracellular neural cAMP
CC stimulators or intracellular neural Ca 2+ enhancers. The invention is
CC useful for modulating neurogenesis in neural tissue of a patient
CC exhibiting at least one symptom of central nervous system disorder, such

CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,
CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,
CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,
CC spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord
CC injury, cancer-related brain and spinal cord injury, multi-infarct
CC dementia and geriatric dementia; for increasing the intracellular levels
CC of or stimulating cAMP levels in a cell (preferably a cell from a neural
CC tissue); and for in vitro modulation of neurogenesis. The agent modulates
CC neurogenesis in neural tissue by modulating proliferation,
CC differentiation, migration or survival of neural stem cells or progenitor
CC cells in the tissue; by maintaining or increasing the amount or
CC percentage of doublecortin positive cells in the neural tissue relative
CC to a patient not dosed with the agent or by activation of a G-protein
CC coupled receptor in the neural tissue. The method results in elevation of
CC cAMP levels of the neural stem cells by over 20% compared to untreated
CC tissue. The in vivo induction of neurogenesis allows treatment of
CC disorders caused by cell loss, injury or disease by endogenous
CC replacement and obviates the need for transplanting foreign cells into a
CC patient. Neurogenesis can also be induced by administration of the
CC neurogenesis-modulating agent directly into a desired site, which avoids
CC unnecessary systemic administration and possible side effects and further
CC provides an alternative to the use of drugs and the controversial use of
CC large quantities of embryonic tissue for treatment of Parkinson's
CC disease. The present sequence is that of a polypeptide which has been
CC shown to have the ability to increase intracellular cAMP levels and which
CC is related to the method of the invention.
XX
SQ Sequence 31 AA;

Query Match 75.0%; Score 57; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 7 HQIYQFTDKD 16

RESULT 9
AAB91768
ID AAB91768 standard; peptide; 40 AA.
XX
AC AAB91768;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:944.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 502; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 40 AA;

Query Match 75.0%; Score 57; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 16 HQIYQFTDKD 25

RESULT 10
AAE09819
ID AAE09819 standard; peptide; 50 AA.
XX
AC AAE09819;
XX
DT 29-NOV-2001 (first entry)
XX
DE Rat adrenomedullin peptide.
XX
KW Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.
XX
OS Rattus sp.
XX
PN US6268474-B1.
XX
PD 31-JUL-2001.
XX
PF 30-APR-1998; 98US-00070504.
XX
PR 30-APR-1998; 98US-00070504.
XX
PA (UYCR-) UNIV CREIGHTON.
XX
PI Smith DD, Saha S, Abel PW;
XX
DR WPI; 2001-564216/63.
XX
PT Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT receptor activity.
XX
PS Claim 5; Col 25-26; 24pp; English.
XX
CC The invention relates to antagonists of the vasoactive peptide calcitonin
CC gene related peptide (CGRP) and other members of the CGRP superfamily.
CC The invention also relates to amino the terminal modifications of
CC peptides to improve their ability to bind to a member of the CGRP-
CC receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC activity which can be used in vitro e.g. in assays to identify and/or
CC isolate CGRP receptors or with intact cells either in vitro or in vivo to

```
CC   inhibit the effect of CGRP binding to its receptor. The present sequence
CC   is rat adrenomedullin peptide
XX
SQ   Sequence 50 AA;

  Query Match             75.0%;  Score 57;  DB 4;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         26 HQIYQFTDKD 35


RESULT 11
ADE51616
ID   ADE51616 standard; protein; 50 AA.
XX
AC   ADE51616;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Adrenomedullin protein #2.
XX
KW   vasoactive; calcitonin gene related peptide; CGRP; migraine; diabetes;
KW   sepsis; inflammation; cardiac disorder; vasodilator; adrenomedullin; rat.
XX
OS   Rattus sp.
XX
PN   US2002068814-A1.
XX
PD   06-JUN-2002.
XX
PF   20-MAR-2001; 2001US-00813345.
XX
PR   30-APR-1998;   98US-00070504.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Smith DD,  Saha S,  Abel PW;
XX
DR   WPI; 2003-874533/81.
XX
PT   New modified vasoactive calcitonin related gene peptides (CGRP), useful
PT   in the treatment of migraines and cardiac disorders, and in the
PT   identification of CGRP antagonists.
XX
PS   Claim 7; SEQ ID NO 15; 26pp; English.
XX
CC   The invention relates to a new modified vasoactive peptide. The
CC   vasoactive peptides are useful in inhibiting calcitonin gene related
CC   peptide CGRP binding to one or more receptors, identifying CGRP
CC   antagonists, and identifying a CGRP receptor in a cell. The peptides are
CC   also useful in treating migraine, diabetes, sepsis, inflammation, cardiac
CC   disorders, and acts as a potent vasodilator. The present sequence
CC   represents the amino acid sequence of an adrenomedullin protein.
XX
SQ   Sequence 50 AA;

  Query Match             75.0%;  Score 57;  DB 7;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         26 HQIYQFTDKD 35


RESULT 12
AAB91765
ID   AAB91765 standard; peptide; 52 AA.
XX
AC   AAB91765;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:941.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW   blood component; modification; succinimidyl; maleimido group; amino;
KW   hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200069900-A2.
XX
PD   23-NOV-2000.
XX
PF   17-MAY-2000; 2000WO-US013576.
XX
PR   17-MAY-1999;   99US-0134406P.
PR   10-SEP-1999;   99US-0153406P.
PR   15-OCT-1999;   99US-0159783P.
XX
PA   (CONJ-) CONJUCHEM INC.
XX
PI   Bridon DP,  Ezrin AM,  Milner PG,  Holmes DL,  Thibaudeau K;
XX
DR   WPI; 2001-112059/12.
XX
PT   Modifying and attaching therapeutic peptides to albumin prevents
PT   peptidase degradation, useful for increasing length of in vivo activity.
XX
PS   Disclosure; Page 501; 733pp; English.
XX
CC   The present invention describes a modified therapeutic peptide (I)
CC   comprising a therapeutically active amino acid region (III) and a
CC   reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC   a less therapeutically active amino acid region (IV), which covalently
CC   bonds with amino/hydroxyl/thiol groups on blood components to form a
CC   peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC   (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC   factors and neurotransmitters, to protect them from peptidase activity in
CC   vivo for the treatment of various disorders. Endogenous therapeutic
CC   peptides are not suitable as drug candidates as they require frequent
CC   administration due to rapid degradation by peptidases in the body.
CC   Modifying and attaching therapeutic peptides to albumin prevents or
CC   reduces the action of peptidases to increase length of activity (half
CC   life) and specificity as bonding to large molecules decreases
CC   intracellular uptake and interference with physiological processes.
CC   AAB90829 to AAB92441 represent peptides which can be used in the
CC   exemplification of the present invention
XX
SQ   Sequence 52 AA;

  Query Match             75.0%;  Score 57;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         27 HQIYQFTDKD 36


RESULT 13
AAB91759
ID   AAB91759 standard; peptide; 52 AA.
XX
AC   AAB91759;
XX
DT   22-JUN-2001  (first entry)
XX
DE   Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW   Protection; endogenous therapeutic peptide; peptidase; conjugation;
```

KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 498; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 28 HQIYQFTDKD 37

RESULT 14
AAB75110
ID AAB75110 standard; protein; 52 AA.
XX
AC AAB75110;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human adrenomedullin (AM) protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP007023.
XX
PR 15-OCT-1999; 99JP-00294147.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19806.
XX
PT Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host.
XX
PS Disclosure; Page 45; 75pp; Japanese.
XX
CC The present invention describes a method (M1) for producing
CC adrenomedullin precursor. The method comprises: (a) producing the fused
CC protein using a recombinant host cell; (b) restricted digestion of the
CC fused protein by a protease followed by collection of sediment; and (c)
CC dissolving the sediment and extracting adrenomedullin precursor. The
CC method can be used for the production of adrenomedullin precursor for
CC pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and
CC AAB75110 to AAB75124 represent sequences which are used in the
CC exemplification of the present invention
XX
SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 28 HQIYQFTDKD 37

RESULT 15
AAE09818
ID AAE09818 standard; peptide; 52 AA.
XX
AC AAE09818;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human adrenomedullin peptide #1.
XX
KW Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.
XX
OS Homo sapiens.
XX
PN US6268474-B1.
XX
PD 31-JUL-2001.
XX
PF 30-APR-1998; 98US-00070504.
XX
PR 30-APR-1998; 98US-00070504.
XX
PA (UYCR-) UNIV CREIGHTON.
XX
PI Smith DD, Saha S, Abel PW;
XX
DR WPI; 2001-564216/63.
XX
PT Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT receptor activity.
XX
PS Claim 5; Col 25-26; 24pp; English.

XX
CC The invention relates to antagonists of the vasoactive peptide calcitonin
CC gene related peptide (CGRP) and other members of the CGRP superfamily.
CC The invention also relates to amino the terminal modifications of
CC peptides to improve their ability to bind to a member of the CGRP-
CC receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC activity which can be used in vitro e.g. in assays to identify and/or
CC isolate CGRP receptors or with intact cells either in vitro or in vivo to
CC inhibit the effect of CGRP binding to its receptor. The present sequence
CC is human adrenomedullin peptide
XX
SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         28 HQIYQFTDKD 37
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Search completed: January 5, 2005, 08:49:13
Job time : 69.0682 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 10.0455 Seconds
(without alignments)
85.823 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76	100.0	13	3	US-09-011-922A-2	Sequence 2, Appli
2	57	75.0	13	4	US-09-280-501-15	Sequence 15, Appl
3	57	75.0	26	4	US-09-280-501-1	Sequence 1, Appli
4	57	75.0	27	4	US-09-280-501-2	Sequence 2, Appli
5	57	75.0	28	4	US-09-280-501-3	Sequence 3, Appli
6	57	75.0	29	4	US-09-280-501-4	Sequence 4, Appli
7	57	75.0	30	4	US-09-280-501-5	Sequence 5, Appli
8	57	75.0	31	3	US-09-070-504-23	Sequence 23, Appl
9	57	75.0	31	3	US-09-011-922A-3	Sequence 3, Appli
10	57	75.0	31	3	US-09-011-922A-14	Sequence 14, Appl
11	57	75.0	31	4	US-09-280-501-9	Sequence 9, Appli
12	57	75.0	31	4	US-09-813-345C-23	Sequence 23, Appl
13	57	75.0	38	4	US-09-280-501-6	Sequence 6, Appli
14	57	75.0	40	4	US-09-280-501-8	Sequence 8, Appli
15	57	75.0	40	4	US-09-280-501-11	Sequence 11, Appl
16	57	75.0	50	3	US-09-070-504-15	Sequence 15, Appl
17	57	75.0	50	4	US-09-280-501-7	Sequence 7, Appli
18	57	75.0	50	4	US-09-813-345C-15	Sequence 15, Appl
19	57	75.0	52	3	US-09-070-504-14	Sequence 14, Appl
20	57	75.0	52	4	US-09-813-345C-14	Sequence 14, Appl
21	57	75.0	185	1	US-08-233-389C-1	Sequence 1, Appli
22	57	75.0	185	2	US-08-801-863-1	Sequence 1, Appli
23	57	75.0	185	2	US-08-486-596A-1	Sequence 1, Appli
24	57	75.0	185	2	US-09-004-713-1	Sequence 1, Appli
25	57	75.0	188	1	US-08-233-389C-3	Sequence 3, Appli
26	57	75.0	188	2	US-08-801-863-3	Sequence 3, Appli
27	57	75.0	188	2	US-08-486-596A-3	Sequence 3, Appli
28	57	75.0	188	2	US-09-004-713-3	Sequence 3, Appli
29	44	57.9	23	4	US-09-280-501-17	Sequence 17, Appl
30	44	57.9	70	4	US-09-248-796A-21094	Sequence 21094, A
31	44	57.9	514	4	US-09-266-965-116	Sequence 116, App
32	41	53.9	264	4	US-09-252-991A-19737	Sequence 19737, A
33	41	53.9	317	4	US-09-634-238-241	Sequence 241, App
34	41	53.9	519	4	US-08-956-171E-5230	Sequence 5230, Ap
35	41	53.9	519	4	US-08-781-986A-5230	Sequence 5230, Ap
36	40	52.6	157	4	US-09-252-991A-25900	Sequence 25900, A
37	39	51.3	433	4	US-09-252-991A-21838	Sequence 21838, A
38	39	51.3	686	3	US-09-368-169-8	Sequence 8, Appli
39	38.5	50.7	374	3	US-09-306-881-2	Sequence 2, Appli
40	38.5	50.7	396	4	US-09-107-532A-5962	Sequence 5962, Ap
41	38	50.0	370	4	US-09-134-000C-4746	Sequence 4746, Ap
42	38	50.0	408	4	US-09-270-767-60172	Sequence 60172, A
43	38	50.0	418	4	US-09-107-532A-6073	Sequence 6073, Ap
44	38	50.0	586	4	US-09-583-110-3470	Sequence 3470, Ap
45	38	50.0	598	4	US-09-270-767-44718	Sequence 44718, A

ALIGNMENTS

RESULT 1
US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  13 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      NAME/KEY:  P071
;      OTHER INFORMATION:  YGG-PreproAM (122-131)
US-09-011-922A-2

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  Best Local Similarity   100.0%;  Pred. No. 1.5e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGGHQIYQFTDKD 13
              |||||||||||||
Db          1 YGGHQIYQFTDKD 13


RESULT 2
US-09-280-501-15
; Sequence 15, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-15

  Query Match             75.0%;  Score 57;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.0023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          1 HQIYQFTDKD 10


RESULT 3
US-09-280-501-1
; Sequence 1, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-1

  Query Match             75.0%;  Score 57;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.0049;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          2 HQIYQFTDKD 11


RESULT 4
US-09-280-501-2
; Sequence 2, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-2

  Query Match             75.0%;  Score 57;  DB 4;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.0051;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          3 HQIYQFTDKD 12


RESULT 5
US-09-280-501-3
; Sequence 3, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-3

  Query Match             75.0%;  Score 57;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          4 HQIYQFTDKD 13
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RESULT 6
US-09-280-501-4
; Sequence 4, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 29
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-4

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          5 HQIYQFTDKD 14


RESULT 7
US-09-280-501-5
; Sequence 5, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-5

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          6 HQIYQFTDKD 15


RESULT 8
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
;  GENERAL INFORMATION:
;    APPLICANT:  Smith, Derek D.
;    APPLICANT:  Saha, Shankar
;    APPLICANT:  Abel, Peter W.
;    TITLE OF INVENTION:  PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;    TITLE OF INVENTION:  SUPERFAMILY AND METHODS OF USE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mueting, Raasch & Gebhardt, P.A.
;      STREET:  119 No. 6268474th Fourth Street
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,504
;      FILING DATE:  30-APR-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCormack, Myra H
;      REGISTRATION NUMBER:  36,602
;      REFERENCE/DOCKET NUMBER:  180.00020101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/305-1220
;      TELEFAX:  612/305-1228
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-070-504-23

  Query Match             75.0%;  Score 57;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.0059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 9
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
;  GENERAL INFORMATION:
;    APPLICANT:  Cuttitta, Frank; Martinez,
;    APPLICANT:  Alfredo; Miller, Mae Jean; Unsworth, Edward
;    APPLICANT:  J.; Hook, William; Walsh, Thomas; Grey,
;    APPLICANT:  Karen; Macri, Charles
;    TITLE OF INVENTION:  Functional Role of
;    TITLE OF INVENTION:  Adrenomedullin (AM) and the Gene-Related
;    TITLE OF INVENTION:  Product (PAMP) in Human Pathology and
;    TITLE OF INVENTION:  Physiology
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS WORD 97
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,922A
;      FILING DATE:  17-Feb-1998
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,514
;      FILING DATE:  18-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,936
;      FILING DATE:  30-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/013,172
;      FILING DATE:  12-Mar-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/13286
;      FILING DATE:  16-Aug-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leslie A. Serunian
;      REGISTRATION NUMBER:  35,353
;      REFERENCE/DOCKET NUMBER:  2026-4202US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      NAME/KEY:  P072
;      OTHER INFORMATION:  PreproAM(116-146)
US-09-011-922A-3

  Query Match             75.0%;  Score 57;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.0059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 10
US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
;  GENERAL INFORMATION:
;    APPLICANT:  Cuttitta, Frank; Martinez,
;    APPLICANT:  Alfredo; Miller, Mae Jean; Unsworth, Edward
;    APPLICANT:  J.; Hook, William; Walsh, Thomas; Grey,
;    APPLICANT:  Karen; Macri, Charles
;    TITLE OF INVENTION:  Functional Role of
;    TITLE OF INVENTION:  Adrenomedullin (AM) and the Gene-Related
;    TITLE OF INVENTION:  Product (PAMP) in Human Pathology and
;    TITLE OF INVENTION:  Physiology
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS WORD 97
;      SOFTWARE:  ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/011,922A
;      FILING DATE:  17-Feb-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,514
;      FILING DATE:  18-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/002,936
;      FILING DATE:  30-Aug-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/60/013,172
;      FILING DATE:  12-Mar-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/13286
;      FILING DATE:  16-Aug-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Leslie A. Serunian
;      REGISTRATION NUMBER:  35,353
;      REFERENCE/DOCKET NUMBER:  2026-4202US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      OTHER INFORMATION:  Synthetic homolog of
;      OTHER INFORMATION:  two-thirds of the intact AM peptide
US-09-011-922A-14

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  Best Local Similarity   100.0%;  Pred. No. 0.0059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
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Db          7 HQIYQFTDKD 16


RESULT 11
US-09-280-501-9
; Sequence 9, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-9

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  Best Local Similarity   100.0%;  Pred. No. 0.0059;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          7 HQIYQFTDKD 16


RESULT 12
US-09-813-345C-23
; Sequence 23, Application US/09813345C
; Patent No. 6756205
; GENERAL INFORMATION:
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;  APPLICANT: CREIGHTON UNIVERSITY
;  APPLICANT:  SMITH, Derek D.
;  APPLICANT:  SAHA, Shankar
;  APPLICANT:  ABEL, Peter W.
;  TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 180.00020102
;  CURRENT APPLICATION NUMBER: US/09/813,345C
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: 09/070,504
;  PRIOR FILING DATE: 1998-04-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificially Synthesized Peptide
US-09-813-345C-23

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
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Db          7 HQIYQFTDKD 16


RESULT 13
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; Sequence 6, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
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; SEQ ID NO 6
;   LENGTH: 38
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US-09-280-501-6

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Qy          4 HQIYQFTDKD 13
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Db         14 HQIYQFTDKD 23


RESULT 14
US-09-280-501-8
; Sequence 8, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-280-501-8

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Qy          4 HQIYQFTDKD 13
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RESULT 15
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; Sequence 11, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
;  APPLICANT: Cooper, Garth James Smith
;  APPLICANT:  Reid, Ian Reginald
;  APPLICANT:  Cornish, Jillian
;  TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
;  TITLE OF INVENTION:  ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
;  FILE REFERENCE: 08987-005001
;  CURRENT APPLICATION NUMBER: US/09/280,501
;  CURRENT FILING DATE:  1999-03-30
;  PRIOR APPLICATION NUMBER: 08/634,562
;  PRIOR FILING DATE: 1996-04-18
;  NUMBER OF SEQ ID NOS: 17
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; SEQ ID NO 11
;   LENGTH: 40
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;   ORGANISM: Homo sapiens
US-09-280-501-11

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Search completed: January  5, 2005, 08:45:18
Job time : 11.0455 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:44:46 ; Search time 229.864 Seconds
(without alignments)
20.344 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	57	75.0	31	9	US-09-931-700-3	Sequence 3, Appli
3	57	75.0	31	9	US-09-931-700-14	Sequence 14, Appl
4	57	75.0	31	9	US-09-813-345-23	Sequence 23, Appl
5	57	75.0	50	9	US-09-813-345-15	Sequence 15, Appl
6	57	75.0	52	9	US-09-813-345-14	Sequence 14, Appl
7	57	75.0	52	14	US-10-197-954-2	Sequence 2, Appli
8	57	75.0	52	15	US-10-360-101-74	Sequence 74, Appl
9	57	75.0	52	16	US-10-474-635A-19	Sequence 19, Appl
10	57	75.0	185	14	US-10-364-889-6	Sequence 6, Appli
11	57	75.0	185	15	US-10-372-683-12	Sequence 12, Appl
12	57	75.0	185	16	US-10-675-406A-7	Sequence 7, Appli
13	57	75.0	185	16	US-10-755-889-148	Sequence 148, App
14	45	59.2	117	17	US-10-425-115-194068	Sequence 194068,
15	44	57.9	157	15	US-10-424-599-207877	Sequence 207877,
16	44	57.9	514	10	US-09-953-348-116	Sequence 116, App
17	44	57.9	514	14	US-10-267-255-116	Sequence 116, App
18	44	57.9	833	14	US-10-027-000-2	Sequence 2, Appli
19	44	57.9	2384	15	US-10-335-977-8087	Sequence 8087, Ap
20	44	57.9	2440	15	US-10-335-977-8088	Sequence 8088, Ap
21	42	55.3	107	15	US-10-424-599-211456	Sequence 211456,
22	42	55.3	324	14	US-10-369-493-16979	Sequence 16979, A
23	41.5	54.6	488	14	US-10-369-493-9990	Sequence 9990, Ap
24	41	53.9	151	16	US-10-767-701-59836	Sequence 59836, A
25	41	53.9	164	17	US-10-425-115-239182	Sequence 239182,
26	41	53.9	317	15	US-10-264-213-147	Sequence 147, App
27	41	53.9	519	8	US-08-781-986A-5230	Sequence 5230, Ap
28	41	53.9	519	15	US-10-329-624-5230	Sequence 5230, Ap
29	41	53.9	1234	16	US-10-437-963-137236	Sequence 137236,
30	40	52.6	55	17	US-10-425-115-254064	Sequence 254064,
31	40	52.6	63	17	US-10-425-115-345298	Sequence 345298,
32	40	52.6	177	16	US-10-767-701-53889	Sequence 53889, A
33	40	52.6	261	15	US-10-335-977-7714	Sequence 7714, Ap
34	40	52.6	279	15	US-10-425-114-44570	Sequence 44570, A
35	40	52.6	281	15	US-10-335-977-7715	Sequence 7715, Ap
36	40	52.6	308	17	US-10-425-115-367230	Sequence 367230,
37	40	52.6	593	15	US-10-425-114-43323	Sequence 43323, A
38	40	52.6	666	16	US-10-437-963-108953	Sequence 108953,
39	40	52.6	675	15	US-10-424-599-229257	Sequence 229257,
40	40	52.6	720	17	US-10-425-115-275151	Sequence 275151,
41	40	52.6	952	16	US-10-437-963-115492	Sequence 115492,
42	40	52.6	1849	15	US-10-276-774-2188	Sequence 2188, Ap
43	40	52.6	1905	15	US-10-259-194A-86	Sequence 86, Appl
44	39	51.3	112	15	US-10-424-599-253952	Sequence 253952,
45	39	51.3	116	15	US-10-424-599-176774	Sequence 176774,

ALIGNMENTS

RESULT 1
US-09-931-700-2
; Sequence 2, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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;   OTHER INFORMATION: Description of Artificial Sequence: Peptide,
;   OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)
US-09-931-700-2

  Query Match             100.0%;  Score 76;  DB 9;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-06;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YGGHQIYQFTDKD 13
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Db          1 YGGHQIYQFTDKD 13


RESULT 2
US-09-931-700-3
; Sequence 3, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
;  APPLICANT: CUTTITTA, FRANK
;  APPLICANT:  MARTINEZ, ALFREDO
;  APPLICANT:  MILLER, MAE JEAN
;  APPLICANT:  UNSWORTH, EDWARD J.
;  APPLICANT:  HOOK, WILLIAM
;  APPLICANT:  WALSH, THOMAS
;  APPLICANT:  GREY, KAREN
;  APPLICANT:  MACRI, CHARLES
;  TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
;  TITLE OF INVENTION:  Gene-Related Product (PAMP) in Human Pathology and
;  TITLE OF INVENTION:  Physiology
;  FILE REFERENCE: 2026-4202US4
;  CURRENT APPLICATION NUMBER: US/09/931,700
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/011,922
;  PRIOR FILING DATE: 1998-02-17
;  PRIOR APPLICATION NUMBER: PCT/US96/13286
;  PRIOR FILING DATE: 1996-08-16
;  PRIOR APPLICATION NUMBER: US/60/013,172
;  PRIOR FILING DATE: 1996-03-12
;  PRIOR APPLICATION NUMBER: US60/002,936
;  PRIOR FILING DATE: 1995-08-30
;  PRIOR APPLICATION NUMBER: US/60/002,514
;  PRIOR FILING DATE: 1995-08-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
;   OTHER INFORMATION: PreproAM (amino acids 116-146)
US-09-931-700-3

  Query Match             75.0%;  Score 57;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 3
US-09-931-700-14
; Sequence 14, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
;  APPLICANT: CUTTITTA, FRANK
;  APPLICANT:  MARTINEZ, ALFREDO
;  APPLICANT:  MILLER, MAE JEAN
;  APPLICANT:  UNSWORTH, EDWARD J.
;  APPLICANT:  HOOK, WILLIAM
;  APPLICANT:  WALSH, THOMAS
;  APPLICANT:  GREY, KAREN
;  APPLICANT:  MACRI, CHARLES
;  TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
;  TITLE OF INVENTION:  Gene-Related Product (PAMP) in Human Pathology and
;  TITLE OF INVENTION:  Physiology
;  FILE REFERENCE: 2026-4202US4
;  CURRENT APPLICATION NUMBER: US/09/931,700
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/011,922
;  PRIOR FILING DATE: 1998-02-17
;  PRIOR APPLICATION NUMBER: PCT/US96/13286
;  PRIOR FILING DATE: 1996-08-16
;  PRIOR APPLICATION NUMBER: US/60/013,172
;  PRIOR FILING DATE: 1996-03-12
;  PRIOR APPLICATION NUMBER: US60/002,936
;  PRIOR FILING DATE: 1995-08-30
;  PRIOR APPLICATION NUMBER: US/60/002,514
;  PRIOR FILING DATE: 1995-08-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide,
;   OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino
;   OTHER INFORMATION: acid sequence representing two-thirds of the
;   OTHER INFORMATION: intact AM peptide
US-09-931-700-14

  Query Match             75.0%;  Score 57;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db          7 HQIYQFTDKD 16


RESULT 4
US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
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;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

  Query Match             75.0%;  Score 57;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
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Db          7 HQIYQFTDKD 16


RESULT 5
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; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-813-345-15

  Query Match             75.0%;  Score 57;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.035;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         26 HQIYQFTDKD 35


RESULT 6
US-09-813-345-14
; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 52 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-813-345-14

  Query Match             75.0%;  Score 57;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0.036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         28 HQIYQFTDKD 37


RESULT 7
US-10-197-954-2
; Sequence 2, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
;  APPLICANT: K"ster, Hubert
;  APPLICANT:  Siddiqi, Suhaib
;  APPLICANT:  Little, Daniel
;  TITLE OF INVENTION: Capture Compounds, Collections Thereof
;  TITLE OF INVENTION:  And Methods For Analyzing The Proteome And Complex
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 24743-2305
;  CURRENT APPLICATION NUMBER: US/10/197,954
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 60/306,019
;  PRIOR FILING DATE: 2001-07-16
;  PRIOR APPLICATION NUMBER: 60/314,123
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/363,433
;  PRIOR FILING DATE: 2002-03-11
```

```
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-197-954-2

  Query Match            75.0%;  Score 57;  DB 14;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 0.036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         28 HQIYQFTDKD 37


RESULT 8
US-10-360-101-74
; Sequence 74, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
;  APPLICANT: Moll, Gert  N.
;  APPLICANT:  Leenhouts, Cornelis J.
;  TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
;  FILE REFERENCE: 2183-5673
;  CURRENT APPLICATION NUMBER: US/10/360,101
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: EP 02077060.8
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 309
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide
US-10-360-101-74

  Query Match            75.0%;  Score 57;  DB 15;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 0.036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         28 HQIYQFTDKD 37


RESULT 9
US-10-474-635A-19
; Sequence 19, Application US/10474635A
; Publication No. US20040176567A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Innovation Ltd
;  TITLE OF INVENTION: Peptides
;  FILE REFERENCE: 480821.00004
;  CURRENT APPLICATION NUMBER: US/10/474,635A
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: GB 0109438.2
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-474-635A-19

  Query Match            75.0%;  Score 57;  DB 16;  Length 52;
  Best Local Similarity  100.0%;  Pred. No. 0.036;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db         28 HQIYQFTDKD 37


RESULT 10
US-10-364-889-6
; Sequence 6, Application US/10364889
; Publication No. US20030224989A1
; GENERAL INFORMATION:
;  APPLICANT: Pahel, Gregory L.
;  APPLICANT:  Quinn, Kerry
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Osteoarthritis
;  FILE REFERENCE: 21402-558
;  CURRENT APPLICATION NUMBER: US/10/364,889
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,376
;  PRIOR FILING DATE: 2002-02-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-889-6

  Query Match            75.0%;  Score 57;  DB 14;  Length 185;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131


RESULT 11
US-10-372-683-12
; Sequence 12, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 12
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-12

  Query Match            75.0%;  Score 57;  DB 15;  Length 185;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131


RESULT 12
US-10-675-406A-7
; Sequence 7, Application US/10675406A
; Publication No. US20040121375A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer Pharmaceuticals Corporation
```

; APPLICANT: Eveleigh, Deepa
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: METHODS FOR PREDICTION AND PROGNOSIS OF CANCER, AND MONITORING
; TITLE OF INVENTION: CANCER THERAPY
; FILE REFERENCE: 5138
; CURRENT APPLICATION NUMBER: US/10/675,406A
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/415,194
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-675-406A-7

Query Match 75.0%; Score 57; DB 16; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 122 HQIYQFTDKD 131

RESULT 13
US-10-755-889-148
; Sequence 148, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-148

Query Match 75.0%; Score 57; DB 16; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 122 HQIYQFTDKD 131

RESULT 14
US-10-425-115-194068
; Sequence 194068, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 194068
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(117)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_108570C.1.pep
US-10-425-115-194068

Query Match 59.2%; Score 45; DB 17; Length 117;
Best Local Similarity 63.6%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGGHQIYQFTD 11
||| |:| | |
Db 44 YGGEQVYNFDD 54

RESULT 15
US-10-424-599-207877
; Sequence 207877, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207877
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(157)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2973C.1.pep
US-10-424-599-207877

Query Match 57.9%; Score 44; DB 15; Length 157;
Best Local Similarity 53.8%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGGHQIYQFTDKD 13
|| | :|| :||
Db 103 YGEHNVYQAREKD 115

Search completed: January 5, 2005, 09:15:07
Job time : 229.864 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 14.1818 Seconds
(without alignments)
88.199 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	75.0	185	2	JN0684	adrenomedullin pre
2	57	75.0	185	2	JN0766	adrenomedullin pre
3	57	75.0	188	2	S41600	adrenomedullin - p
4	51	67.1	643	2	S76069	hypothetical prote
5	45	59.2	776	2	T02702	hypothetical prote
6	44	57.9	2231	2	D71870	hypothetical prote
7	42	55.3	280	2	H70089	hypothetical prote
8	42	55.3	324	2	A87544	hypothetical prote
9	42	55.3	350	2	T21106	hypothetical prote
10	42	55.3	563	2	T09378	hypothetical prote
11	41	53.9	185	2	C86705	hypothetical prote
12	41	53.9	467	2	T21690	hypothetical prote
13	41	53.9	514	2	D89775	hypothetical prote
14	40	52.6	146	2	G83445	conserved hypothet
15	40	52.6	260	2	H71979	probable type II r
16	40	52.6	275	2	T32005	hypothetical prote
17	39.5	52.0	606	2	T40556	hypothetical prote
18	39	51.3	176	2	B35697	transcription fact
19	39	51.3	310	2	H69986	hypothetical prote
20	39	51.3	444	1	E69130	histidine-tRNA lig
21	39	51.3	705	2	JX0194	prolyl oligopeptid
22	39	51.3	1356	2	S51389	ROM2 protein - yea
23	38.5	50.7	322	2	T22410	hypothetical prote
24	38	50.0	165	2	F69819	conserved hypothet
25	38	50.0	254	2	B70860	probable enoyl-CoA
26	38	50.0	257	2	AH0859	periplasmic fimbri
27	38	50.0	264	2	T23866	hypothetical prote
28	38	50.0	387	2	T28402	ORF MSV241 leucine
29	38	50.0	391	2	H89859	hypothetical prote
30	38	50.0	425	2	S17759	protein kinase, ca
31	38	50.0	532	2	T14335	protein kinase, ca
32	38	50.0	564	2	A96999	pectate lyase rela
33	38	50.0	571	2	S58356	pepT protein - Sta
34	38	50.0	586	2	A95167	ABC transporter, A
35	38	50.0	586	2	H98032	hypothetical prote
36	38	50.0	952	2	E84534	hypothetical prote
37	38	50.0	1337	2	T30291	dextranase - Strep
38	37.5	49.3	569	2	JS0101	alpha-amylase (EC
39	37	48.7	105	2	T26838	hypothetical prote
40	37	48.7	164	2	AG0539	probable lipoprote
41	37	48.7	227	2	H82344	rfbT protein VC025
42	37	48.7	250	2	B86817	oxidoreductase ypi
43	37	48.7	253	2	F90507	sugar phosphate nu
44	37	48.7	257	2	E82238	imidazoleglycerol-
45	37	48.7	285	2	T29832	hypothetical prote

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, T.
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869; PMID:8074714
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: UNIPROT:P35318; GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g76533
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenomedu
A;Reference number: JN0684; MUID:93343928; PMID:7688224
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocyto
A;Reference number: JN0476; MUID:93249425; PMID:8387282
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following g

Query Match 75.0%; Score 57; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131
```

RESULT 2
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621; PMID:7690563
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Cross-references: UNIPROT:P43145
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

```
  Query Match             75.0%;  Score 57;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 0.016;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        119 HQIYQFTDKD 128
```

RESULT 3
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encc
A;Reference number: S41600; MUID:94139945; PMID:8043068
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: UNIPROT:P53366; GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

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  Query Match             75.0%;  Score 57;  DB 2;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131
```

RESULT 4
S76069
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76069
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-643 <KAN>
A;Cross-references: UNIPROT:Q55549; EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA1004
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

```
  Query Match             67.1%;  Score 51;  DB 2;  Length 643;
  Best Local Similarity   72.7%;  Pred. No. 0.69;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GHQIYQFTDKD 13
              ||:|||:|| |
Db        447 GHEIYQYTDPD 457
```

RESULT 5
T02702
hypothetical protein At2g03240 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T18E12.9
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02702; A84446
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron
submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.
A;Reference number: Z14702
A;Accession: T02702
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-776 <ROU>
A;Cross-references: UNIPROT:O81050; EMBL:AC005313; NID:g3548797; PID:g3548806
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-776 <STO>
A;Cross-references: GB:AE002093; NID:g3548806; PIDN:AAC34478.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g03240
A;Map position: 2
A;Introns: 219/1; 340/2; 387/1; 417/2; 503/3; 538/3; 603/3; 698/3; 744/2
A;Note: T18E12.9

```
  Query Match             59.2%;  Score 45;  DB 2;  Length 776;
  Best Local Similarity   66.7%;  Pred. No. 9.4;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GGHQIYQFTDKD 13
              |||||  |:| |
Db         84 GGHQIGHFSDSD 95
```

RESULT 6
D71870
hypothetical protein jhp0928 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71870

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71870
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2231 <ARN>
A;Cross-references: UNIPROT:Q9ZKK7; GB:AE001522; GB:AE001439; NID:g4155505; PIDN:AAD0650
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0928

Query Match 57.9%; Score 44; DB 2; Length 2231;
Best Local Similarity 53.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 YGGHQIYQFTDKD 13
              || |:||   ||:
Db        620 YGNHKIYSSNDKE 632
```

RESULT 7
H70089
hypothetical protein yycI - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H70089
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H70089
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-280 <KUN>
A;Cross-references: UNIPROT:Q45612; GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16075.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yycI
C;Superfamily: Bacillus subtilis hypothetical protein yycI

Query Match 55.3%; Score 42; DB 2; Length 280;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 YGGHQIYQFTD 11
              | || ||| ||
Db        152 YEGHYIYQKTD 162
```

RESULT 8
A87544
hypothetical protein CC2378 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87544
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: UNIPROT:Q9A5R9; GB:AE005673; NID:g13423911; PIDN:AAK24349.1; GSPDB:
C;Genetics:
A;Gene: CC2378
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology

Query Match 55.3%; Score 42; DB 2; Length 324;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 GGHQIYQFTDKD 13
              |||::|   | |
Db        244 GGHEVYNIGDND 255
```

RESULT 9
T21106
hypothetical protein F19B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21106
R;Thomas, K.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19375
A;Accession: T21106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-350 <WIL>
A;Cross-references: UNIPROT:Q19582; EMBL:Z69635; NID:g1200023; PIDN:CAA93458.1; GSPDB:G
A;Experimental source: clone F19B6
C;Genetics:
A;Gene: CESP:F19B6.3
A;Map position: 4
A;Introns: 180/3; 274/2

Query Match 55.3%; Score 42; DB 2; Length 350;
Best Local Similarity 46.2%; Pred. No. 13;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 YGGHQIYQFTDKD 13
              | | :|: ||::|
Db         20 YNGRKIFDFTERD 32
```

RESULT 10
T09378
hypothetical protein F23K16.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09378; T04999
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16652
A;Accession: T09378
A;Molecule type: DNA
A;Residues: 1-563 <BEV>
A;Cross-references: UNIPROT:Q9SV96; EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250
A;Experimental source: cultivar Columbia; BAC clone F23K16
R;Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15394
A;Accession: T04999
A;Molecule type: DNA
A;Residues: 444-563 <BE2>
A;Cross-references: EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
C;Genetics:

A;Gene: ATSP:F23K16.250
A;Map position: 4
A;Introns: 118/3; 502/3
A;Note: T19P19.10

Query Match 55.3%; Score 42; DB 2; Length 563;
Best Local Similarity 58.3%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 GGHQIYQFTDKD 13
              ||:|: :| |||
Db        491 GGNQLTEFQDKD 502
```

RESULT 11
C86705
hypothetical protein ygdA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86705
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86705
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-185 <STO>
A;Cross-references: UNIPROT:Q9CHS8; GB:AE005176; PID:g12723547; PIDN:AAK04741.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ygdA

Query Match 53.9%; Score 41; DB 2; Length 185;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 GHQIYQFTDKD 13
              ||  | ||| |
Db        154 GHDFYVFTDAD 164
```

RESULT 12
T21690
hypothetical protein F33A8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21690
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19459
A;Accession: T21690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-467 <WIL>
A;Cross-references: UNIPROT:O62214; EMBL:Z81525; PIDN:CAB04258.1; GSPDB:GN00020; CESP:F3
A;Experimental source: clone F33A8
C;Genetics:
A;Gene: CESP:F33A8.4
A;Map position: 2
A;Introns: 29/3; 159/2; 212/3; 243/3; 266/3; 365/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F33A8.4

Query Match 53.9%; Score 41; DB 2; Length 467;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 YGGHQIYQFTDK 12
              | ||::|| ::|
Db        368 YEGHKLYQHSEK 379
```

RESULT 13
D89775
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89775
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89775
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-514 <KUR>
A;Cross-references: UNIPROT:Q99X71; GB:BA000018; PID:g13700060; PIDN:BAB41359.1; GSPDB:(
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0139

Query Match 53.9%; Score 41; DB 2; Length 514;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 GGHQIYQFTDKD 13
              || || ||: ||
Db        449 GGRQIGQFSSKD 460
```

RESULT 14
G83445
conserved hypothetical protein PA1607 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83445
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: UNIPROT:Q9I3B4; GB:AE004588; GB:AE004091; NID:g9947563; PIDN:AAG049
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1607

Query Match 52.6%; Score 40; DB 2; Length 146;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 GGHQIYQFTDK 12
              | || |: |||
Db         75 GSHQEYRLTDK 85
```

RESULT 15
H71979
probable type II restriction enzyme - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: H71979
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.,
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: H71979
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-260 <ARN>
A;Cross-references: UNIPROT:Q9ZN14; GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD0562
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0046

Query Match 52.6%; Score 40; DB 2; Length 260;
Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 YGGHQIYQFTD 11
              :||||  || |
Db        194 FGGHQNAQFND 204
```

Search completed: January 5, 2005, 08:44:39
Job time : 16.1818 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 75.0455 Seconds
(without alignments)
99.671 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	75.0	27	2	Q9TRZ6	Q9trz6 sus scrofa
2	57	75.0	185	1	ADML_HUMAN	P35318 homo sapien
3	57	75.0	185	1	ADML_RAT	P43145 rattus norv
4	57	75.0	185	2	AAP35548	Aap35548 homo sapi
5	57	75.0	185	2	AAH61775	Aah61775 rattus no
6	57	75.0	188	1	ADML_PIG	P53366 sus scrofa
7	52	68.4	188	1	ADML_BOVIN	O62827 bos taurus
8	52	68.4	188	1	ADML_CANFA	O77559 canis famil
9	52	68.4	188	2	Q95KP0	Q95kp0 bos taurus
10	51	67.1	184	1	ADML_MOUSE	P97297 mus musculu
11	51	67.1	184	2	AAH52665	Aah52665 mus muscu
12	51	67.1	643	2	Q55549	Q55549 synechocyst
13	45.5	59.9	388	2	Q24544	Q24544 drosophila
14	45.5	59.9	488	2	Q8INM4	Q8inm4 drosophila
15	45.5	59.9	488	2	AAN13464	Aan13464 drosophil
16	45.5	59.9	537	2	Q8INM6	Q8inm6 drosophila
17	45.5	59.9	980	1	SYN_DROME	Q24546 drosophila
18	45.5	59.9	981	2	Q86BA0	Q86ba0 drosophila
19	45.5	59.9	981	2	AAO41538	Aao41538 drosophil
20	45	59.2	776	2	O81050	O81050 arabidopsis
21	45	59.2	823	2	Q6R8G5	Q6r8g5 arabidopsis
22	45	59.2	823	2	AAR99487	Aar99487 arabidops
23	44	57.9	514	2	Q9X5R9	Q9x5r9 streptomyce
24	44	57.9	833	2	Q7Z9M4	Q7z9m4 trichoderma
25	44	57.9	2231	2	Q9ZKK7	Q9zkk7 helicobacte
26	43.5	57.2	611	2	Q7Q0H2	Q7q0h2 anopheles g
27	43.5	57.2	611	2	Q7Q9C9	Q7q9c9 anopheles g
28	42	55.3	173	2	Q8MXJ0	Q8mxj0 caenorhabdi
29	42	55.3	184	2	Q9EWQ4	Q9ewq4 streptomyce
30	42	55.3	280	2	Q45612	Q45612 bacillus su
31	42	55.3	324	2	Q9A5R9	Q9a5r9 caulobacter
32	42	55.3	326	2	Q8RCV8	Q8rcv8 thermoanaer
33	42	55.3	350	2	Q19582	Q19582 caenorhabdi
34	42	55.3	563	2	Q9SV96	Q9sv96 arabidopsis
35	42	55.3	1206	2	Q9UTT2	Q9utt2 schizosacch
36	41	53.9	185	2	Q9L474	Q9l474 lactococcus
37	41	53.9	185	2	Q9CHS8	Q9chs8 lactococcus
38	41	53.9	245	2	Q7V1T4	Q7v1t4 prochloroco
39	41	53.9	330	2	Q7N9F6	Q7n9f6 photorhabdu
40	41	53.9	392	2	Q88XD7	Q88xd7 lactobacill
41	41	53.9	467	2	O62214	O62214 caenorhabdi
42	41	53.9	478	2	Q7US57	Q7us57 rhodopirell
43	41	53.9	514	2	Q6GCY0	Q6gcy0 staphylococ
44	41	53.9	514	2	Q6GKG1	Q6gkg1 staphylococ
45	41	53.9	514	2	Q8NYQ7	Q8nyq7 staphylococ

ALIGNMENTS

RESULT 1
Q9TRZ6
ID Q9TRZ6 PRELIMINARY; PRT; 27 AA.
AC Q9TRZ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ADRENOMEDULLIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96157714; PubMed=8576091;
RA Ichiki Y., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.;
RT "Distribution and characterization of immunoreactive adrenomedullin in porcine tissue, and isolation of adrenomedullin [26-52] and adrenomedullin [34-52] from porcine duodenum.";
RL J. Biochem. 118:765-770(1995).
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin; 1.
DR PRINTS; PR00801; ADRENOMEDULN.
SQ SEQUENCE 27 AA; 3063 MW; B8DC7FA18D8B3D90 CRC64;

Query Match 75.0%; Score 57; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
||||||||||
Db 3 HQIYQFTDKD 12

RESULT 2
ADML_HUMAN
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN Name=ADM; Synonyms=AM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;

```
RA   Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT   "Cloning and characterization of cDNA encoding a precursor for human
RT   adrenomedullin.";
RL   Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=94354869; PubMed=8074714;
RA   Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA   Kitamura K., Eto T., Matsuo H.;
RT   "Genomic structure of human adrenomedullin gene.";
RL   Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [5]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [6]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445;
RA   Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents. Numerous actions have been reported most related to the
CC       physiologic control of fluid and electrolyte homeostasis. In the
CC       kidney, am is diuretic and natriuretic, and both am and pamp
CC       inhibit aldosterone secretion by direct adrenal actions. In
CC       pituitary gland, both peptides at physiologically relevant doses
CC       inhibit basal ACTH secretion. Both peptides appear to act in brain
CC       and pituitary gland to facilitate the loss of plasma volume,
CC       actions which complement their hypotensive effects in blood
CC       vessels.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highest levels found in pheochromocytoma and
CC       adrenal medulla. Also found in lung, ventricle and kidney tissues.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; BC015961; AAH15961.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JC2351; JN0684.
DR   Genew; HGNC:259; ADM.
DR   MIM; 103275; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0006171; P:cAMP biosynthesis; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0008015; P:circulation; TAS.
DR   GO; GO:0007565; P:pregnancy; TAS.
DR   GO; GO:0006701; P:progesterone biosynthesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Polymorphism; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE       22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP        45     92
FT   PEPTIDE       95    146       Adrenomedullin.
FT   PROPEP       148    185       PreproAM C-terminal fragment.
FT   DISULFID     110    115
FT   MOD_RES       41     41       Arginine amide (G-42 provides amide
FT                                  group).
FT   MOD_RES      146    146       Tyrosine amide (G-147 provides amide
FT                                  group).
FT   VARIANT       50     50       S -> R (in dbSNP:5005).
FT                                  /FTId=VAR_014861.
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

  Query Match             75.0%;  Score 57;  DB 1;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131


RESULT 3
ADML_RAT
ID   ADML_RAT       STANDARD;      PRT;   185 AA.
AC   P43145;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=Adm;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX   MEDLINE=93384621; PubMed=7690563;
RA   Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA   Matsuo H., Eto T.;
```

```
RT   "Molecular cloning and biological activities of rat adrenomedullin, a
RT   hypotensive peptide.";
RL   Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96102137; PubMed=8524787;
RA   Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA   Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT   "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT   its role in exacerbating focal brain ischemic damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in adrenal glands, lung, kidney,
CC       heart, spleen, duodenum and submandibular glands.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   PIR; JN0766; JN0766.
DR   RGD; 2047; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL       1     21       By similarity.
FT   PEPTIDE      22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45    91       By similarity.
FT   PEPTIDE      94    143      Adrenomedullin.
FT   PROPEP       149   185      PreproAM C-terminal fragment (By
FT                               similarity).
FT   DISULFID     107   112      By similarity.
FT   MOD_RES      41    41       Arginine amide (G-42 provides amide
FT                               group) (By similarity).
FT   MOD_RES      143   143      Tyrosine amide (G-144 provides amide
FT                               group) (By similarity).
SQ   SEQUENCE   185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;

  Query Match             75.0%;  Score 57;  DB 1;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        119 HQIYQFTDKD 128


RESULT 4
AAP35548
ID   AAP35548    PRELIMINARY;      PRT;   185 AA.
AC   AAP35548;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT006902; AAP35548.1; -.
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

  Query Match             75.0%;  Score 57;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131


RESULT 5
AAH61775
ID   AAH61775    PRELIMINARY;      PRT;   185 AA.
AC   AAH61775;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061775; AAH61775.1; -.
SQ   SEQUENCE   185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;

  Query Match             75.0%;  Score 57;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        119 HQIYQFTDKD 128


RESULT 6
ADML_PIG
ID   ADML_PIG       STANDARD;      PRT;   188 AA.
AC   P53366;
```

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DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM; Synonyms=AM;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning of
RT   cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]
RP   SEQUENCE OF 22-41.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin N-
RT   terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adrenal glands, lung and
CC       kidney.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D14875; BAA03590.1; -.
DR   PIR; S41600; S41600.
DR   InterPro; IPR001710; Adrenomedullin.
DR   InterPro; IPR011038; Calycin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE       22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP        45    92
FT   PEPTIDE       95    146      Adrenomedullin.
FT   PROPEP        153   188      PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID      110   115      By similarity.
FT   MOD_RES       41    41       Arginine amide (G-42 provides amide
FT                                group).
FT   MOD_RES       146   146      Tyrosine amide (G-147 provides amide
FT                                group).
SQ   SEQUENCE   188 AA;  20893 MW;  71749460F5660A61 CRC64;

  Query Match             75.0%;  Score 57;  DB 1;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 0.066;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||||||||
Db        122 HQIYQFTDKD 131


RESULT 7
```

```
ADML_BOVIN
ID   ADML_BOVIN     STANDARD;      PRT;   188 AA.
AC   O62827;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: Hypotensive peptide. May function as a hormone in
CC       circulation control (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE       22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP        45    92       By similarity.
FT   PEPTIDE       95    146      Adrenomedullin.
FT   PROPEP        148   188      PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID      110   115      By similarity.
FT   MOD_RES       41    41       Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES       146   146      Tyrosine amide (G-147 provides amide
FT                                group) (By similarity).
SQ   SEQUENCE   188 AA;  20981 MW;  3002E79AB3B6612C CRC64;

  Query Match             68.4%;  Score 52;  DB 1;  Length 188;
  Best Local Similarity   90.0%;  Pred. No. 0.52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              |||| |||||
Db        122 HQIYHFTDKD 131


RESULT 8
ADML_CANFA
ID   ADML_CANFA     STANDARD;      PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM;
OS   Canis familiaris (Dog).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99002704; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF045773; AAD05423.1; -.
DR   EMBL; U96127; AAD09957.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92       By similarity.
FT   PEPTIDE      95    146       Adrenomedullin.
FT   PROPEP      148    188       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID     110    115      By similarity.
FT   MOD_RES       41     41      Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES      146    146      Tyrosine amide (G-147 provides amide
FT                                group) (By similarity).
FT   CONFLICT     130    130      N -> K (in Ref. 2).
SQ   SEQUENCE   188 AA;  20929 MW;  809D6A64F98F5578 CRC64;

  Query Match             68.4%;  Score 52;  DB 1;  Length 188;
  Best Local Similarity   90.0%;  Pred. No. 0.52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              |||||||| |
Db        122 HQIYQFTDND 131


RESULT 9
Q95KP0
ID   Q95KP0      PRELIMINARY;      PRT;   188 AA.
AC   Q95KP0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Adrenomedullin.
GN   Name=pBAM-2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21630318; PubMed=11754956;
RA   Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RA   Kangawa K., Eto T.;
RT   "Adrenomedullin (11-26): a novel endogenous hypertensive peptide
RT   isolated from bovine adrenal medulla.";
RL   Peptides 22:1713-1718(2001).
DR   EMBL; AB055107; BAB62176.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
SQ   SEQUENCE   188 AA;  20963 MW;  6102E69A756DCA86 CRC64;

  Query Match             68.4%;  Score 52;  DB 2;  Length 188;
  Best Local Similarity   90.0%;  Pred. No. 0.52;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              |||| |||||
Db        122 HQIYHFTDKD 131


RESULT 10
ADML_MOUSE
ID   ADML_MOUSE     STANDARD;      PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=Adm;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99046755; PubMed=9808778;
RA   Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
RA   Ko M.S.H.;
RT   "Expression of adrenomedullin, a hypotensive peptide, in the
RT   trophoblast giant cells at the embryo implantation site in mouse.";
RL   Dev. Biol. 203:264-275(1998).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
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DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92       By similarity.
FT   PEPTIDE      95    144       Adrenomedullin.
FT   PROPEP      151    184       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID     108    113      By similarity.
FT   MOD_RES       41     41      Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES      144    144      Tyrosine amide (G-145 provides amide
FT                                group) (By similarity).
FT   CONFLICT     173    173      A -> G (in Ref. 2).
SQ   SEQUENCE   184 AA;  20764 MW;  C88C99045A79C898 CRC64;

  Query Match             67.1%;  Score 51;  DB 1;  Length 184;
  Best Local Similarity   90.0%;  Pred. No. 0.77;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||| ||||
Db        120 HQIYQLTDKD 129


RESULT 11
AAH52665
ID   AAH52665    PRELIMINARY;      PRT;   184 AA.
AC   AAH52665;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Egg;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Egg;
RA   Strausberg R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC052665; AAH52665.1; -.
SQ   SEQUENCE   184 AA;  20750 MW;  C88C9903C479C898 CRC64;

  Query Match             67.1%;  Score 51;  DB 2;  Length 184;
  Best Local Similarity   90.0%;  Pred. No. 0.77;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HQIYQFTDKD 13
              ||||| ||||
Db        120 HQIYQLTDKD 129


RESULT 12
Q55549
ID   Q55549      PRELIMINARY;      PRT;   643 AA.
AC   Q55549;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Slr0168 protein.
GN   OrderedLocusNames=slr0168;
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC6803;
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
DR   EMBL; D63999; BAA10047.1; -.
DR   PIR; S76069; S76069.
KW   Complete proteome.
SQ   SEQUENCE   643 AA;  68369 MW;  1EE9001D3332B411 CRC64;

  Query Match             67.1%;  Score 51;  DB 2;  Length 643;
  Best Local Similarity   72.7%;  Pred. No. 2.9;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GHQIYQFTDKD 13
              ||:|||:|| |
Db        447 GHEIYQYTDPD 457


RESULT 13
Q24544
ID   Q24544      PRELIMINARY;      PRT;   388 AA.
AC   Q24544;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Homologous to synapsin II (Fragment).
GN   Name=Syn; Synonyms=SYN2;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=wildtype 'Berlin'; TISSUE=Head;
RX   MEDLINE=96209149; PubMed=8627354;
RA   Klagges B.R., Heimbeck G., Godenschwege T.A., Hofbauer A.,
RA   Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
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RA   Buchner E.;
RT   "Invertebrate synapsins: a single gene codes for several isoforms in
RT   Drosophila.";
RL   J. Neurosci. 16:3154-3165(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=wildtype 'Berlin'; TISSUE=Head;
RA   Klagges B.R.E.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X95454; CAA64724.1; -.
DR   FlyBase; FBgn0004575; Syn.
DR   GO; GO:0008021; C:synaptic vesicle; IEA.
DR   GO; GO:0007269; P:neurotransmitter secretion; IEA.
DR   InterPro; IPR001359; Synapsin.
DR   Pfam; PF02750; Synapsin_C; 1.
DR   Pfam; PF02078; Synapsin_N; 1.
DR   PRINTS; PR01368; SYNAPSIN.
FT   NON_TER       1       1
SQ   SEQUENCE   388 AA;  42887 MW;  583B24E6456CBF40 CRC64;

  Query Match             59.9%;  Score 45.5;  DB 2;  Length 388;
  Best Local Similarity   52.6%;  Pred. No. 17;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    7;  Gaps    1;

Qy         1 YGG-------HQIYQFTDK 12
             |||       | |||| ||
Db        81 YGGVPSINSLHSIYQFQDK 99


RESULT 14
Q8INM4
ID   Q8INM4      PRELIMINARY;      PRT;   488 AA.
AC   Q8INM4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CG3985-PC.
GN   Name=Syn; ORFNames=CG3985;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FLYBASE;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003686; AAN13464.2; -.
DR   HSSP; P17599; 1AUX.
DR   FlyBase; FBgn0004575; Syn.
DR   GO; GO:0008021; C:synaptic vesicle; IEA.
DR   GO; GO:0007269; P:neurotransmitter secretion; IEA.
DR   InterPro; IPR001359; Synapsin.
DR   Pfam; PF02750; Synapsin_C; 1.
DR   Pfam; PF02078; Synapsin_N; 1.
DR   PRINTS; PR01368; SYNAPSIN.
SQ   SEQUENCE   488 AA;  52962 MW;  452EDAAD4C26241E CRC64;

  Query Match             59.9%;  Score 45.5;  DB 2;  Length 488;
  Best Local Similarity   52.6%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    7;  Gaps    1;

Qy         1 YGG-------HQIYQFTDK 12
             |||       | |||| ||
Db       181 YGGVPSINSLHSIYQFQDK 199
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RESULT 15
AAN13464
ID   AAN13464    PRELIMINARY;      PRT;   488 AA.
AC   AAN13464;
DT   01-APR-2004 (TrEMBLrel. 27, Created)
DT   01-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CG3985-PC.
GN   SYN OR CG3985.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003686; AAN13464.2; -.
DR   FlyBase; FBgn0004575; Syn.
SQ   SEQUENCE   488 AA;  52962 MW;  452EDAAD4C26241E CRC64;

  Query Match             59.9%;  Score 45.5;  DB 2;  Length 488;
  Best Local Similarity   52.6%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    7;  Gaps    1;

Qy          1 YGG-------HQIYQFTDK 12
              |||       | |||| ||
Db        181 YGGVPSINSLHSIYQFQDK 199


Search completed: January  5, 2005, 08:43:46
Job time : 78.0455 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:23 ; Search time 159.932 Seconds
(without alignments)
69.533 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	100.0	31	2	AAW25160	Aaw25160 Human pre
2	163	100.0	31	4	AAB91762	Aab91762 Adrenomed
3	163	100.0	31	4	AAE09827	Aae09827 Human adr
4	163	100.0	31	7	ADC25153	Adc25153 Human ang
5	163	100.0	31	8	ADP18403	Adp18403 Neurogene
6	163	100.0	52	4	AAB91759	Aab91759 Adrenomed
7	163	100.0	52	4	AAB75110	Aab75110 Human adr
8	163	100.0	52	4	AAE09818	Aae09818 Human adr
9	163	100.0	52	6	ABP55104	Abp55104 Human adr
10	163	100.0	52	7	ADC25152	Adc25152 Human ang
11	163	100.0	52	7	ADG91993	Adg91993 Human mat
12	163	100.0	52	8	ADL91994	Adl91994 Adrenomed
13	163	100.0	52	8	ADM94034	Adm94034 Human AM
14	163	100.0	52	8	ADN03278	Adn03278 Exemplary
15	163	100.0	52	8	ADM98309	Adm98309 Mature hu
16	163	100.0	52	8	ADP18429	Adp18429 Neurogene
17	163	100.0	52	8	ADP18402	Adp18402 Neurogene
18	163	100.0	53	4	AAB75111	Aab75111 Glycine e
19	163	100.0	53	4	AAB75112	Aab75112 Glycine e
20	163	100.0	53	6	ABJ18665	Abj18665 Universal
21	163	100.0	62	4	AAB75113	Aab75113 Linker pe
22	163	100.0	91	8	ADF55556	Adf55556 Active hu
23	163	100.0	120	4	AAB75123	Aab75123 UspA(1-56
24	163	100.0	120	4	AAB75122	Aab75122 UspA(1-57
25	163	100.0	120	6	ABJ18669	Abj18669 Universal
26	163	100.0	120	6	ABJ18670	Abj18670 Universal
27	163	100.0	147	4	AAB75124	Aab75124 UspA(1-84
28	163	100.0	147	6	ABJ18671	Abj18671 Universal
29	163	100.0	170	4	AAB75114	Aab75114 Thioredox
30	163	100.0	185	4	AAB60344	Aab60344 Human adr
31	163	100.0	185	4	AAB49697	Aab49697 Human adr
32	163	100.0	185	6	ABP72347	Abp72347 Adrenomed
33	163	100.0	185	7	ADA27595	Ada27595 Human adr
34	163	100.0	185	8	ADF55557	Adf55557 Human adr
35	163	100.0	185	8	ADN10849	Adn10849 Human adr
36	163	100.0	185	8	ADM98308	Adm98308 Human pre
37	163	100.0	185	8	ADP19855	Adp19855 Human pre
38	163	100.0	185	8	ADP12587	Adp12587 Protein e
39	163	100.0	185	8	ADO36937	Ado36937 Human pro
40	163	100.0	186	7	ADD18582	Add18582 Human dis
41	163	100.0	206	6	ABJ18668	Abj18668 Universal
42	161	98.8	31	7	ADE51624	Ade51624 Adrenomed
43	157	96.3	52	7	ADE51615	Ade51615 Adrenomed
44	157	96.3	188	4	AAB60345	Aab60345 Porcine a
45	157	96.3	188	4	AAB49698	Aab49698 Porcine a

ALIGNMENTS

RESULT 1
AAW25160
ID AAW25160 standard; peptide; 31 AA.
XX
AC AAW25160;
XX
DT 08-DEC-1997 (first entry)
XX
DE Human preproadrenomedullin derived immunogen, PO72.
XX
KW Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
KW skin; blood related; disease; type II diabetes; preeclampsia;
KW neurotransmission regulation; allergy; mast cell degranulation;
KW antibacterial; antifungal; wound repair.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .31
FT /note= "residues 116-146 of preproadrenomedullin"
FT Modified-site 31
FT /note= "amidated"
XX
PN WO9707214-A1.
XX
PD 27-FEB-1997.
XX
PF 16-AUG-1996; 96WO-US013286.
XX
PR 18-AUG-1995; 95US-0002514P.
PR 30-AUG-1995; 95US-0002936P.
PR 12-MAR-1996; 96US-0013172P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cuttitta F, Martinez A, Miller MJ, Unsworth EJ, Hook W, Walsh T;
PI Gray K, Macri C;
XX
DR WPI; 1997-165298/15.
XX
PT Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used in
PT the diagnosis and treatment of type II diabetes and cancer.
XX
PS Claim 1; Page 43; 106pp; English.
XX
CC Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20 were used
CC for the production of anti-AM antibodies (Ab). PO70 represents preproAM
CC amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at the N-

CC terminus, PO71 represents preproAM aa 122-131 with the sequence Tyr-Gly-
CC Gly attached at the N-terminus, PO72 represents preproAM aa 116-146 and
CC PAMP-20 represents the proAM N-terminus. The Ab are useful for the
CC prevention and/or treatment of cancers, e.g. adrenal, nervous system,
CC lung, colon, ovarian and breast cancer by inhibiting cell growth. They
CC are also useful for regulating insulin secretion and blood glucose
CC metabolism and therefore for treating and/or preventing diabetes type II.
CC They may be used for the diagnosis or treatment of conditions relating to
CC pregnancy e.g. preeclampsia. The Ab are also useful for the following:
CC (i) regulating neurotransmission or neuron growth in areas of the central
CC nervous system; (ii) lessening or inhibiting mast cell degranulation and
CC hence reducing the effects of an allergic response; (iii) inhibiting or
CC preventing bacterial and fungal growth (to treat infection); (iv)
CC facilitating wound healing; and (v) promoting organ and bone development
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Db 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 2
AAB91762
ID AAB91762 standard; peptide; 31 AA.
XX
AC AAB91762;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:938.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 499-500; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Db 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 3
AAE09827
ID AAE09827 standard; peptide; 31 AA.
XX
AC AAE09827;
XX
DT 29-NOV-2001 (first entry)
XX
DE Human adrenomedullin peptide #2.
XX
KW Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW CGRP-receptor identification; adrenomedullin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 31
FT /note= "C-terminal amide"
XX
PN US6268474-B1.
XX
PD 31-JUL-2001.
XX
PF 30-APR-1998; 98US-00070504.
XX
PR 30-APR-1998; 98US-00070504.
XX
PA (UYCR-) UNIV CREIGHTON.
XX
PI Smith DD, Saha S, Abel PW;
XX
DR WPI; 2001-564216/63.
XX
PT Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT receptor activity.
XX
PS Claim 5; Col 6; 24pp; English.
XX
CC The invention relates to antagonists of the vasoactive peptide calcitonin
CC gene related peptide (CGRP) and other members of the CGRP superfamily.
CC The invention also relates to amino the terminal modifications of
CC peptides to improve their ability to bind to a member of the CGRP-
CC receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC activity which can be used in vitro e.g. in assays to identify and/or
CC isolate CGRP receptors or with intact cells either in vitro or in vivo to
CC inhibit the effect of CGRP binding to its receptor. The present sequence
CC is human adrenomedullin peptide
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 4
ADC25153
ID   ADC25153 standard; peptide; 31 AA.
XX
AC   ADC25153;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human angiogenesis inhibiting peptide #SEQ ID 2.
XX
KW   Cytostatic; gene therapy; cancer; stomach; colon; pulmonary; ovarian;
KW   liver; pancreatic; human.
XX
OS   Homo sapiens.
XX
PN   WO2003078460-A1.
XX
PD   25-SEP-2003.
XX
PF   19-MAR-2003; 2003WO-JP003344.
XX
PR   19-MAR-2002; 2002JP-00075575.
XX
PA   (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE CO.
XX
PI   Kobayashi M;
XX
DR   WPI; 2003-767505/72.
XX
PT   Peptides with effect on inhibiting angiogenesis in cancer cells and
PT   inhibiting proliferation of cancer cells, and encoded polynucleotides,
PT   applicable in drug compositions for treating cancer.
XX
PS   Example 2; SEQ ID NO 2; 41pp; Japanese.
XX
CC   The invention relates to peptides comprising an amino acid sequence
CC   derived from a fully defined 52 amino acid sequence (S1) given in the
CC   specification. Peptides may be created by deletion of some amino acids
CC   from the N-terminal of S1. The peptides are applicable in drug
CC   compositions for treating cancer e.g. stomach cancer, colon cancer,
CC   pulmonary cancer, ovarian cancer, liver cancer or pancreatic cancer. The
CC   current sequence represents an angiogenesis inhibiting peptide of the
CC   invention.
XX
SQ   Sequence 31 AA;

  Query Match             100.0%;  Score 163;  DB 7;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||||||||||||||||||||||||||||||
Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 5
ADP18403
ID   ADP18403 standard; peptide; 31 AA.
XX
AC   ADP18403;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Neurogenesis modulation-related peptide SeqID17.
XX
KW   neurogenesis modulation; neural tissue; central nervous system disorder;
KW   neurodegenerative; ischaemic; learning and memory disorder;
KW   neurological trauma; nootropic; neuroprotective; CNS-Gen;
KW   cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;
KW   haemostatic; hypertensive; muscular-Gen; ophthalmological;
KW   antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;
KW   neural stem cell; progenitor cell;
KW   neural tissue G-protein coupled receptor activator; neurogenesis inducer;
KW   intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;
KW   intracellular neural Ca 2+ enhancer; Parkinson's disease;
KW   Parkinson's disorder; Huntington's disease; Alzheimer's disease;
KW   multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;
KW   progressive supranuclear palsy; Lewy body disease; spinal ischaemia;
KW   ischaemic stroke; cerebral infarction; spinal cord injury;
KW   cancer-related brain; spinal cord injury; multi-infarct dementia;
KW   geriatric dementia; cAMP level; embryonic tissue; human.
XX
OS   Homo sapiens.
XX
PN   WO2004045592-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-IB005311.
XX
PR   20-NOV-2002; 2002US-0427912P.
XX
PA   (NEUR-) NEURONOVA AB.
PA   (BERT/) BERTILSSON G.
PA   (ERLA/) ERLANDSSON R.
PA   (FRIS/) FRISEN J.
PA   (HAEG/) HAEGESTRAND A.
PA   (HEID/) HEIDRICH J.
PA   (HELL/) HELLSTROEM K.
PA   (HAEG/) HAEGGBLAD J.
PA   (JANS/) JANSSON K.
PA   (KORT/) KORTESMAA J.
PA   (LIND/) LINDQUIST P.
PA   (LUND/) LUNDH H.
PA   (MCGU/) MCGUIRE J.
PA   (MERC/) MERCER A.
PA   (NJBE/) NJBERG K.
PA   (OSSO/) OSSOINAK A.
PA   (PATR/) PATRONE C.
PA   (ROEN/) ROENNHOLM H.
PA   (ZACH/) ZACHRISSON O.
PA   (WIKS/) WIKSTROEM L.
XX
PI   Bertilsson G,  Erlandsson R,  Frisen J,  Haegestrand A,  Heidrich J;
PI   Hellstroem K,  Haeggblad J,  Jansson K,  Kortesmaa J,  Lindquist P;
PI   Lundh H,  Mcguire J,  Mercer A,  Njberg K,  Ossoinak A,  Patrone C;
PI   Roennholm H,  Zachrisson O,  Wikstroem L;
XX
DR   WPI; 2004-449666/42.
XX
PT   Use of agent(s) that elevate intracellular cyclic adenosine monophosphate
PT   or intracellular calcium levels in neural tissue for modulating
PT   neurogenesis to treat central nervous system disorder.
XX
PS   Disclosure; SEQ ID NO 17; 77pp; English.
XX
CC   This invention relates to a novel method of modulating neurogenesis in
CC   the neural tissue of a patient exhibiting symptom(s) of a central nervous
CC   system disorder, such as neurodegenerative, ischaemic or learning and
CC   memory disorder or neurological trauma. The method involves at least one
CC   agent (A) that elevates intracellular cyclic adenosine monophosphate
CC   (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+
CC   levels in the neural tissue, which is administered where (A) modulates
CC   and (B) induces neurogenesis. The invention may be useful for the
CC   production of compounds with a nootropic, neuroprotective, CNS-Gen,
CC   cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian.
CC   haemostatic, hypertensive, muscular-Gen, ophthalmological,
CC   antiinflammatory, analgesic or antidiabetic activity. These compounds may
CC   act as neurogenesis modulators, neural stem or progenitor cell
CC   proliferation, differentiation and/or migration modulators, neural tissue
```

CC G-protein coupled receptor activators, neurogenesis inducers, intracellular neural cAMP enhancers, intracellular neural cAMP stimulators or intracellular neural Ca 2+ enhancers. The invention is useful for modulating neurogenesis in neural tissue of a patient exhibiting at least one symptom of central nervous system disorder, such as Parkinson's disease and Parkinson's disorders, Huntington's disease, Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis, Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease, spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord injury, cancer-related brain and spinal cord injury, multi-infarct dementia and geriatric dementia; for increasing the intracellular levels of or stimulating cAMP levels in a cell (preferably a cell from a neural tissue); and for in vitro modulation of neurogenesis. The agent modulates neurogenesis in neural tissue by modulating proliferation, differentiation, migration or survival of neural stem cells or progenitor cells in the tissue; by maintaining or increasing the amount or percentage of doublecortin positive cells in the neural tissue relative to a patient not dosed with the agent or by activation of a G-protein coupled receptor in the neural tissue. The method results in elevation of cAMP levels of the neural stem cells by over 20% compared to untreated tissue. The in vivo induction of neurogenesis allows treatment of disorders caused by cell loss, injury or disease by endogenous replacement and obviates the need for transplanting foreign cells into a patient. Neurogenesis can also be induced by administration of the neurogenesis-modulating agent directly into a desired site, which avoids unnecessary systemic administration and possible side effects and further provides an alternative to the use of drugs and the controversial use of large quantities of embryonic tissue for treatment of Parkinson's disease. The present sequence is that of a polypeptide which has been shown to have the ability to increase intracellular cAMP levels and which is related to the method of the invention.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 163; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Db 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

RESULT 6
AAB91759
ID AAB91759 standard; peptide; 52 AA.
XX
AC AAB91759;
XX
DT 22-JUN-2001 (first entry)
XX
DE Adrenomedullin peptide (AM) SEQ ID NO:935.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 498; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 7
AAB75110
ID AAB75110 standard; protein; 52 AA.
XX
AC AAB75110;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human adrenomedullin (AM) protein.
XX
KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
XX
OS Homo sapiens.
XX
PN WO200127310-A1.
XX
PD 19-APR-2001.
XX
PF 10-OCT-2000; 2000WO-JP007023.
XX
PR 15-OCT-1999; 99JP-00294147.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
XX
DR WPI; 2001-282044/29.
DR N-PSDB; AAH19806.
XX
PT Producing adrenomedullin useful for pharmaceutical and diagnostic
PT application comprises producing fused adrenomedullin precursor using a
PT recombinant host.
XX
PS Disclosure; Page 45; 75pp; Japanese.
XX

```
CC   The present invention describes a method (M1) for producing
CC   adrenomedullin precursor. The method comprises: (a) producing the fused
CC   protein using a recombinant host cell; (b) restricted digestion of the
CC   fused protein by a protease followed by collection of sediment; and (c)
CC   dissolving the sediment and extracting adrenomedullin precursor. The
CC   method can be used for the production of adrenomedullin precursor for
CC   pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and
CC   AAB75110 to AAB75124 represent sequences which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 163;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 8
AAE09818
ID   AAE09818 standard; peptide; 52 AA.
XX
AC   AAE09818;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Human adrenomedullin peptide #1.
XX
KW   Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
KW   CGRP-receptor identification; adrenomedullin.
XX
OS   Homo sapiens.
XX
PN   US6268474-B1.
XX
PD   31-JUL-2001.
XX
PF   30-APR-1998;   98US-00070504.
XX
PR   30-APR-1998;   98US-00070504.
XX
PA   (UYCR-) UNIV CREIGHTON.
XX
PI   Smith DD,  Saha S,  Abel PW;
XX
DR   WPI; 2001-564216/63.
XX
PT   Vasoactive peptides useful for inhibiting calcitonin gene related peptide
PT   receptor activity.
XX
PS   Claim 5; Col 25-26; 24pp; English.
XX
CC   The invention relates to antagonists of the vasoactive peptide calcitonin
CC   gene related peptide (CGRP) and other members of the CGRP superfamily.
CC   The invention also relates to amino the terminal modifications of
CC   peptides to improve their ability to bind to a member of the CGRP-
CC   receptor super-family. CGRP antagonists are used for inhibiting CGRP
CC   activity which can be used in vitro e.g. in assays to identify and/or
CC   isolate CGRP receptors or with intact cells either in vitro or in vivo to
CC   inhibit the effect of CGRP binding to its receptor. The present sequence
CC   is human adrenomedullin peptide
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 163;  DB 4;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 9
ABP55104
ID   ABP55104 standard; peptide; 52 AA.
XX
AC   ABP55104;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Human adrenomedullin.
XX
KW   Adrenomedullin; human; protein engineering; solubility; aggregation;
KW   hypotensive; vasodilator; cyclic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  16. .21
XX
PN   WO200283734-A2.
XX
PD   24-OCT-2002.
XX
PF   17-APR-2002; 2002WO-GB001778.
XX
PR   17-APR-2001; 2001GB-00009438.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Zurdo J,  Dobson CM;
XX
DR   WPI; 2003-046916/04.
XX
PT   New modified human calcitonin peptide having reduced aggregation, useful
PT   for the treatment of Paget's disease, hypercalcemia and/or osteoporosis.
XX
PS   Example; Page 21; 35pp; English.
XX
CC   The present sequence is that of human adrenomedullin, a potent
CC   hypotensive and vasodilator. The invention provides modified calcitonin
CC   and related peptides, such as adrenomedullin, that have at least 70%
CC   identity to the native form but are modified such that the tendency of
CC   the peptide to aggregate is reduced. Preferred regions for modification
CC   include those for which the peptide is polymorphic amongst different
CC   species, which increase the propensity of the peptide to form local
CC   interactions of the alpha-helical type, or which reduce the number of
CC   hydrophobic residues or increase the net charge of the peptide. When
CC   aggregation is reduced or prevented, lower doses of the drug can be used.
CC   Side-effects and undesired responses are minimised by retaining high
CC   sequence identity to the human peptide
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 163;  DB 6;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 10
ADC25152
ID   ADC25152 standard; peptide; 52 AA.
XX
AC   ADC25152;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human angiogenesis inhibiting peptide #SEQ ID 1.
```

```
XX
KW   Cytostatic; gene therapy; cancer; stomach; colon; pulmonary; ovarian;
KW   liver; pancreatic; human.
XX
OS   Homo sapiens.
XX
PN   WO2003078460-A1.
XX
PD   25-SEP-2003.
XX
PF   19-MAR-2003; 2003WO-JP003344.
XX
PR   19-MAR-2002; 2002JP-00075575.
XX
PA   (HOKK-) HOKKAIDO TECHNOLOGY LICENSING OFFICE CO.
XX
PI   Kobayashi M;
XX
DR   WPI; 2003-767505/72.
XX
PT   Peptides with effect on inhibiting angiogenesis in cancer cells and
PT   inhibiting proliferation of cancer cells, and encoded polynucleotides,
PT   applicable in drug compositions for treating cancer.
XX
PS   Claim 1; SEQ ID NO 1; 41pp; Japanese.
XX
CC   The invention relates to peptides comprising an amino acid sequence
CC   derived from a fully defined 52 amino acid sequence (S1) given in the
CC   specification. Peptides may be created by deletion of some amino acids
CC   from the N-terminal of S1. The peptides are applicable in drug
CC   compositions for treating cancer e.g. stomach cancer, colon cancer,
CC   pulmonary cancer, ovarian cancer, liver cancer or pancreatic cancer. The
CC   current sequence represents an angiogenesis inhibiting peptide of the
CC   invention.
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 163;  DB 7;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 11
ADG91993
ID   ADG91993 standard; protein; 52 AA.
XX
AC   ADG91993;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human mature adrenomedullin protein.
XX
KW   neuroleptic; antisense therapy; gene therapy; adrenomedullin agonist;
KW   schizophrenia; gene expression; decidual protein induced by progesterone;
KW   DEPP; adrenomedullin; cold shock domain protein A; csdA; antisense;
KW   siRNA; ribozyme; triple helix formation.
XX
OS   Homo sapiens.
XX
PN   WO2003078658-A2.
XX
PD   25-SEP-2003.
XX
PF   19-MAR-2003; 2003WO-EP002875.
XX
PR   20-MAR-2002; 2002US-0366001P.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS PHARMA GMBH.
XX
PI   Buxton FP,  Carpenter WT,  Roberts RC,  Tamminga CA;
XX
DR   WPI; 2003-767532/72.
XX
PT   Screening for schizophrenia in a population utilizing genes encoding the
PT   decidual protein induced by progesterone, adrenomedullin and/or cold
PT   shock domain protein A, useful in diagnosing, preventing and/or treating
PT   schizophrenia.
XX
PS   Disclosure; SEQ ID NO 1; 41pp; English.
XX
CC   The invention relates to a method of screening for schizophrenia in a
CC   population comprises determining the magnitude of expression, in members
CC   of the population, of at least one gene selected from the gene encoding
CC   decidual protein induced by progesterone (DEPP), the gene encoding
CC   adrenomedullin and the gene encoding cold shock domain protein A (csdA)
CC   in a sample, and comparing the magnitude of expression to a baseline of
CC   expression of the gene, where increased gene expression indicates the
CC   presence of schizophrenia. An antisense molecule, siRNA, ribozyme or
CC   nucleic acid molecule promoting triple helix formation that specifically
CC   inhibit the expression of DEPP, csdA or adrenomedullin genes, is useful
CC   for the manufacture of a medicament for the treatment of schizophrenia.
CC   An antibody that specifically binds an epitope of DEPP, csdA or
CC   adrenomedullin is also useful for the manufacture of a medicament for the
CC   treatment of schizophrenia. This sequence represents the mature
CC   adrenomedullin protein.
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 163;  DB 7;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-18;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 12
ADL91994
ID   ADL91994 standard; protein; 52 AA.
XX
AC   ADL91994;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Adrenomedullin hypotensive peptide A13, S16-sequence.
XX
KW   harvesting; recombinant; host cell; N-terminal leader peptide;
KW   pre-peptide; lantibiotic; post-translational modification;
KW   pharmaceuticals; vaccine; immunogenic.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   16
FT                   /note= "This residue forms a thioether bond with residue
FT                   21 to form a lanthionine ring"
FT   Modified-site   21
FT                   /note= "This residue forms a thioether bond with residue
FT                   16 to form a lanthionine ring"
XX
PN   WO2003099862-A1.
XX
PD   04-DEC-2003.
XX
PF   26-MAY-2003; 2003WO-NL000389.
XX
PR   24-MAY-2002; 2002EP-00077060.
PR   07-FEB-2003; 2003US-00360101.
XX
PA   (NANO-) APPLIED NANOSYSTEMS BV.
```

XX
PI Moll GN, Leenhouts CJ, Kuipers OP, Driessen AJM;
XX
DR WPI; 2004-042770/04.
XX
PT Harvesting a desired polypeptide produced by a recombinant host cell, for
PT producing pharmaceuticals, comprises selecting a recombinant nucleic acid
PT comprising nucleic acid fragments encoding a leader peptide and the
PT polypeptide.
XX
PS Claim 4; Page 44; 109pp; English.
XX
CC The invention relates to a novel method for harvesting a (poly)peptide
CC produced by a recombinant host cell. The novel method involves selecting
CC a cell comprising a first nucleic acid encoding a leader peptide and a
CC second nucleic acid fragment encoding the desired (poly)peptide. The
CC first and second fragments are within the same open reading frame of the
CC first nucleic acid and the leader peptide is functionally equivalent to
CC an N-terminal leader peptide found with the pre-peptide of a lantibiotic.
CC The host cells and nucleic acids are useful for producing, harvesting and
CC post-translational modification of polypeptides. The polypeptides may be
CC used in the production of pharmaceuticals, e.g. as antigen for vaccine or
CC immunogenic composition. This sequence represents a polypeptide relating
CC to the novel method of the invention.
XX
SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
||||||||||||||||||||||||||||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 13
ADM94034
ID ADM94034 standard; peptide; 52 AA.
XX
AC ADM94034;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human AM peptide, a CRSP homologue.
XX
KW calcitonin receptor stimulating peptide; CRSP; cAMP activity;
KW skeletal disorder; cancer; hypertension; restenosis; analgesic;
KW appetite suppressant; diuretic; vasotropic; cytostatic; diuretic;
KW osteopathic; anorectic; hypotensive; human; AM.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 16. .21
FT Modified-site 52
FT /note= "C-terminal amide"
XX
PN WO2003102180-A1.
XX
PD 11-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-JP006641.
XX
PR 04-JUN-2002; 2002JP-00162797.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NINA-) JAPAN NAT CARDIOVASCULAR.
XX
PI Minamino N, Katafuchi T;
XX
DR WPI; 2004-043113/04.
XX
PT Calcitonin receptor stimulating peptides promoting cAMP production in
PT cells for treatment of cancer, skeletal disorders and hypertension and as
PT appetite suppressants and analgesics.
XX
PS Disclosure; Fig 2; 62pp; Japanese.
XX
CC This invention relates to novel calcitonin receptor stimulating peptides
CC (CRSPs) that are expressed in the central nervous system and act on the
CC calcitonin receptor to promote the production of cAMP within a cell.
CC Specifically, it refers to CRSPs that can stimulate concentration
CC dependent sodium ion uptake and furthermore act to inhibit calcium ion
CC uptake by the cell. The present invention describes mutant peptides
CC derived from the CRSPs that have additions, deletions and/ or
CC substitutions of one or more amino acids, yet that retain similar
CC activity and are useful for developing drug compositions and
CC pharmaceutically acceptable carriers to treat and/ or prevent skeletal
CC disorders, cancer, hypertension and restenosis. Furthermore, CRSPs can
CC also be used as analgesics, appetite suppressants and diuretics such that
CC exhibit vasotropic, cytostatic, diuretic, osteopathic, anorectic and
CC hypotensive activities. This peptide sequence is a human AM peptide that
CC has cAMP activity, given in an exemplification of the invention.
XX
SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
||||||||||||||||||||||||||||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 14
ADN03278
ID ADN03278 standard; peptide; 52 AA.
XX
AC ADN03278;
XX
DT 17-JUN-2004 (first entry)
XX
DE Exemplary peptide ligand for proteome analysis #2.
XX
KW Peptide ligand; proteome; capture compound; mass spectrometry;
KW protein separation;
KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
XX
OS Unidentified.
XX
PN US2003119021-A1.
XX
PD 26-JUN-2003.
XX
PF 16-JUL-2002; 2002US-00197954.
XX
PR 16-JUL-2001; 2001US-0306019P.
PR 21-AUG-2001; 2001US-0314123P.
PR 11-MAR-2002; 2002US-0363433P.
XX
PA (KOST/) KOSTER H.
PA (SIDD/) SIDDIQI S.
PA (LITT/) LITTLE D P.
XX
PI Koster H, Siddiqi S, Little DP;
XX
DR WPI; 2004-059185/06.
XX
PT Collection of capture compounds capable of binding to biomolecules to
PT form complexes that are stable under mass spectrometry conditions, useful
PT for analysis of biomolecules, especially proteins.
XX
PS Disclosure; SEQ ID NO 2; 165pp; English.
XX

CC The invention relates to a collection of capture compounds capable of
CC binding to biomolecules to form complexes that are stable under mass
CC spectrometry conditions. The formulae for the capture compounds comprises
CC sets of compounds of formula (I)-(III) given in the specification. Also
CC included are analysis of biomolecules (by contacting a composition
CC comprising a biomolecule with the above collection and identifying or
CC detecting bound biomolecules), separating protein conformers (by
CC contacting a composition comprising a biomolecule with the above
CC collection, separating the members of the collection and identifying
CC bound proteins), reducing diversity of a complex mixture of biomolecules
CC (by contacting the mixture with the above collection and separating each
CC set of complexes of capture compounds with biomolecules from the other
CC sets) and identifying phenotype-specific biomolecules (by sorting cells
CC from a single subject into sets according to a phenotype, contacting
CC mixtures of biomolecules from each set with the above collection and
CC comparing the patterns of biomolecule binding from each set). The
CC collection of capture compounds is useful for the analysis of
CC biomolecules, especially proteins (e.g. analysis of a proteome), using
CC mass spectrometry, especially matrix assisted laser desorption ionisation
CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
CC exemplary peptide ligand which may be incorporated into a capture
CC compound of the invention.
XX
SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
||||||||||||||||||||||||||||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

RESULT 15
ADM98309
ID ADM98309 standard; protein; 52 AA.
XX
AC ADM98309;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mature human adrenomedullin protein SeqID 3.
XX
KW AM(11-22); vasoconstriction; human; adrenomedullin; AM; vasoregulatory;
KW blood pressure; vasodilator; vasodilatory shock; septic shock;
KW haemorrhagic shock; vasotropic; hypotensive; immunosuppressive;
KW antibacterial.
XX
OS Homo sapiens.
XX
PN WO2004032708-A2.
XX
PD 22-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031400.
XX
PR 04-OCT-2002; 2002US-0416291P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Cuttitta F, Martinez A, Stetler-Stevenson WG, Unsworth EJ;
PI Saavedra JM;
XX
DR WPI; 2004-340778/31.
XX
PT New AM(11-22) peptides, useful for useful for inducing vasoconstriction,
PT for treating septic shock, vasodilatory shock or hemorrhagic shock, or
PT for reducing blood pressure.
XX
PS Disclosure; SEQ ID NO 3; 40pp; English.
XX
CC This invention relates to a novel peptide AM(11-22) useful for treating
CC shock, or in a pharmaceutical composition for inducing vasoconstriction.
CC Specifically, AM(11-22) is a short peptide derived from human
CC adrenomedullin (AM), which is a vasoregulatory compound that influences
CC blood pressure. The present invention describes screening assays to
CC identify compounds including antibodies, small molecule inhibitors or
CC peptides that modulate AM(11-22)-mediated vasoconstriction and as such
CC represent novel vasodilators or vasoconstrictors. Accordingly, AM(11-22)
CC can be used therapeutically in a pharmaceutical composition to inhibit
CC blood flow following traumatic or surgical injury, as well as for
CC vasodilatory, septic or haemorrhagic shock, and thus exhibits vasotropic,
CC hypotensive, immunosuppressive and antibacterial activities. This
CC polypeptide sequence is the mature human adrenomedullin protein of the
CC invention.
XX
SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
||||||||||||||||||||||||||||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52

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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
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Maximum DB seq length: 2000000000

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Maximum Match 100%
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	163	100.0	31	9	US-09-931-700-3	Sequence 3, Appli
2	163	100.0	31	9	US-09-931-700-14	Sequence 14, Appl
3	163	100.0	31	9	US-09-813-345-23	Sequence 23, Appl
4	163	100.0	52	9	US-09-813-345-14	Sequence 14, Appl
5	163	100.0	52	14	US-10-197-954-2	Sequence 2, Appli
6	163	100.0	52	15	US-10-360-101-74	Sequence 74, Appl
7	163	100.0	52	16	US-10-474-635A-19	Sequence 19, Appl
8	163	100.0	185	14	US-10-364-889-6	Sequence 6, Appli
9	163	100.0	185	15	US-10-372-683-12	Sequence 12, Appl
10	163	100.0	185	16	US-10-675-406A-7	Sequence 7, Appli
11	163	100.0	185	16	US-10-755-889-148	Sequence 148, App
12	148	90.8	50	9	US-09-813-345-15	Sequence 15, Appl
13	57	35.0	13	9	US-09-931-700-2	Sequence 2, Appli
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16	51	31.3	437	15	US-10-389-566-1910	Sequence 1910, Ap
17	50	30.7	425	15	US-10-389-566-1493	Sequence 1493, Ap
18	50	30.7	860	15	US-10-389-566-2131	Sequence 2131, Ap
19	49.5	30.4	352	17	US-10-739-930-5546	Sequence 5546, Ap
20	49	30.1	78	16	US-10-767-701-35785	Sequence 35785, A
21	49	30.1	397	17	US-10-696-616-42	Sequence 42, Appl
22	48	29.4	66	15	US-10-424-599-208178	Sequence 208178,
23	48	29.4	119	15	US-10-424-599-259144	Sequence 259144,
24	48	29.4	168	17	US-10-425-115-346792	Sequence 346792,
25	48	29.4	328	15	US-10-282-122A-77837	Sequence 77837, A
26	48	29.4	380	16	US-10-437-963-195045	Sequence 195045,
27	48	29.4	478	14	US-10-427-631-31	Sequence 31, Appl
28	48	29.4	487	16	US-10-437-963-107189	Sequence 107189,
29	48	29.4	1745	10	US-09-795-061-4	Sequence 4, Appli
30	48	29.4	1745	17	US-10-723-860-2660	Sequence 2660, Ap
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32	47.5	29.1	1058	14	US-10-128-714-8547	Sequence 8547, Ap
33	47	28.8	33	9	US-09-864-761-43882	Sequence 43882, A
34	47	28.8	81	17	US-10-425-115-309562	Sequence 309562,
35	47	28.8	103	16	US-10-437-963-169347	Sequence 169347,
36	47	28.8	327	9	US-09-925-298-570	Sequence 570, App
37	47	28.8	327	14	US-10-102-806-570	Sequence 570, App
38	47	28.8	341	17	US-10-425-115-251952	Sequence 251952,
39	47	28.8	490	15	US-10-424-599-224233	Sequence 224233,
40	47	28.8	590	16	US-10-437-963-139304	Sequence 139304,
41	47	28.8	706	17	US-10-739-930-7483	Sequence 7483, Ap
42	47	28.8	1268	15	US-10-231-956A-494	Sequence 494, App
43	47	28.8	1268	16	US-10-741-601-524	Sequence 524, App
44	47	28.8	1268	16	US-10-741-601-525	Sequence 525, App
45	47	28.8	1268	16	US-10-741-601-526	Sequence 526, App

ALIGNMENTS

RESULT 1
US-09-931-700-3
; Sequence 3, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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;   OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
;   OTHER INFORMATION: PreproAM (amino acids 116-146)
US-09-931-700-3

  Query Match             100.0%;  Score 163;  DB 9;  Length 31;
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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-09-931-700-14
; Sequence 14, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
;  APPLICANT: CUTTITTA, FRANK
;  APPLICANT:  MARTINEZ, ALFREDO
;  APPLICANT:  MILLER, MAE JEAN
;  APPLICANT:  UNSWORTH, EDWARD J.
;  APPLICANT:  HOOK, WILLIAM
;  APPLICANT:  WALSH, THOMAS
;  APPLICANT:  GREY, KAREN
;  APPLICANT:  MACRI, CHARLES
;  TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
;  TITLE OF INVENTION:  Gene-Related Product (PAMP) in Human Pathology and
;  TITLE OF INVENTION:  Physiology
;  FILE REFERENCE: 2026-4202US4
;  CURRENT APPLICATION NUMBER: US/09/931,700
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 09/011,922
;  PRIOR FILING DATE: 1998-02-17
;  PRIOR APPLICATION NUMBER: PCT/US96/13286
;  PRIOR FILING DATE: 1996-08-16
;  PRIOR APPLICATION NUMBER: US/60/013,172
;  PRIOR FILING DATE: 1996-03-12
;  PRIOR APPLICATION NUMBER: US60/002,936
;  PRIOR FILING DATE: 1995-08-30
;  PRIOR APPLICATION NUMBER: US/60/002,514
;  PRIOR FILING DATE: 1995-08-18
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Peptide,
;   OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino
;   OTHER INFORMATION: acid sequence representing two-thirds of the
;   OTHER INFORMATION: intact AM peptide
US-09-931-700-14

  Query Match             100.0%;  Score 163;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-16;
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RESULT 3
US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 31 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

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Db          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31


RESULT 4
US-09-813-345-14
; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
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;              REGISTRATION NUMBER: 36,602
;              REFERENCE/DOCKET NUMBER: 180.00020101
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 612/305-1220
;              TELEFAX: 612/305-1228
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 52 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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RESULT 5
US-10-197-954-2
; Sequence 2, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
;  APPLICANT: K"ster, Hubert
;  APPLICANT:  Siddiqi, Suhaib
;  APPLICANT:  Little, Daniel
;  TITLE OF INVENTION: Capture Compounds, Collections Thereof
;  TITLE OF INVENTION:  And Methods For Analyzing The Proteome And Complex
;  TITLE OF INVENTION:  Compositions
;  FILE REFERENCE: 24743-2305
;  CURRENT APPLICATION NUMBER: US/10/197,954
;  CURRENT FILING DATE:  2002-07-16
;  PRIOR APPLICATION NUMBER: 60/306,019
;  PRIOR FILING DATE: 2001-07-16
;  PRIOR APPLICATION NUMBER: 60/314,123
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/363,433
;  PRIOR FILING DATE: 2002-03-11
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-197-954-2

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Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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RESULT 6
US-10-360-101-74
; Sequence 74, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
;  APPLICANT: Moll, Gert  N.
;  APPLICANT:  Leenhouts, Cornelis J.
;  TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
;  FILE REFERENCE: 2183-5673
;  CURRENT APPLICATION NUMBER: US/10/360,101
;  CURRENT FILING DATE:  2003-02-07
;  PRIOR APPLICATION NUMBER: EP 02077060.8
;  PRIOR FILING DATE: 2002-05-24
;  NUMBER OF SEQ ID NOS: 309
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide
US-10-360-101-74

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Db         22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52


RESULT 7
US-10-474-635A-19
; Sequence 19, Application US/10474635A
; Publication No. US20040176567A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Innovation Ltd
;  TITLE OF INVENTION: Peptides
;  FILE REFERENCE: 480821.00004
;  CURRENT APPLICATION NUMBER: US/10/474,635A
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: GB 0109438.2
;  PRIOR FILING DATE: 2001-04-17
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-474-635A-19

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RESULT 8
US-10-364-889-6
; Sequence 6, Application US/10364889
; Publication No. US20030224989A1
; GENERAL INFORMATION:
;  APPLICANT: Pahel, Gregory L.
;  APPLICANT:  Quinn, Kerry
;  TITLE OF INVENTION: Compositions and Methods for Treatment of Osteoarthritis
;  FILE REFERENCE: 21402-558
;  CURRENT APPLICATION NUMBER: US/10/364,889
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,376
;  PRIOR FILING DATE: 2002-02-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-889-6

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RESULT 9
US-10-372-683-12
; Sequence 12, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 12
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-12

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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 10
US-10-675-406A-7
; Sequence 7, Application US/10675406A
; Publication No. US20040121375A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer Pharmaceuticals Corporation
;  APPLICANT:  Eveleigh, Deepa
;  APPLICANT:  Taylor, Ian
;  TITLE OF INVENTION: METHODS FOR PREDICTION AND PROGNOSIS OF CANCER, AND MONITORING
;  TITLE OF INVENTION:  CANCER THERAPY
;  FILE REFERENCE: 5138
;  CURRENT APPLICATION NUMBER: US/10/675,406A
;  CURRENT FILING DATE:  2003-09-30
;  PRIOR APPLICATION NUMBER: US 60/415,194
;  PRIOR FILING DATE: 2002-09-30
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-675-406A-7

  Query Match             100.0%;  Score 163;  DB 16;  Length 185;
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  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 11
US-10-755-889-148
; Sequence 148, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
;  TITLE OF INVENTION:  PATHWAY
;  FILE REFERENCE: D0284 NP
;  CURRENT APPLICATION NUMBER: US/10/755,889
;  CURRENT FILING DATE:  2004-01-13
;  PRIOR APPLICATION NUMBER: U.S. 60/440,068
;  PRIOR FILING DATE: 2003-01-14
;  PRIOR APPLICATION NUMBER: U.S. 60/469,757
;  PRIOR FILING DATE: 2003-05-12
;  NUMBER OF SEQ ID NOS: 823
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-755-889-148

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Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 12
US-09-813-345-15
; Sequence 15, Application US/09813345
; Patent No. US20020068814A1
;   GENERAL INFORMATION:
;        APPLICANT: Smith, Derek D.
;                   Saha, Shankar
;                   Abel, Peter W.
;        TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;                            SUPERFAMILY AND METHODS OF USE
;        NUMBER OF SEQUENCES: 23
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
;             STREET: 119 No. US20020068814A1th Fourth Street
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55401
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/813,345
;             FILING DATE: 20-Mar-2001
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: McCormack, Myra H
;             REGISTRATION NUMBER: 36,602
;             REFERENCE/DOCKET NUMBER: 180.00020101
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 612/305-1220
;             TELEFAX: 612/305-1228
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-813-345-15
```

Query Match 90.8%; Score 148; DB 9; Length 50;
Best Local Similarity 87.1%; Pred. No. 5.9e-14;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |:|||||||||||||||| :|||:|||||||
Db         20 TMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 50
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RESULT 13
US-09-931-700-2
; Sequence 2, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)
US-09-931-700-2

Query Match 35.0%; Score 57; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 HQIYQFTDKD 16
              ||||||||||
Db          4 HQIYQFTDKD 13
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RESULT 14
US-10-437-963-124471
; Sequence 124471, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 124471
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27206C.1.pep
US-10-437-963-124471

Query Match 32.5%; Score 53; DB 16; Length 67;
Best Local Similarity 41.7%; Pred. No. 5.1;
Matches 10; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

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Qy          8 QIYQFTDKDKDNVAPRSKISPQGY 31
              ::: |    :: ||||| |:|||:
Db         26 KLFWFLTPPRNIVAPRSFIAPQGF 49
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RESULT 15
US-10-424-599-274214
; Sequence 274214, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274214
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89637C.1.pep
US-10-424-599-274214

Query Match 31.3%; Score 51; DB 15; Length 44;
Best Local Similarity 39.3%; Pred. No. 6.2;
Matches 11; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

```
Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISP 28
              | ||: ||  : |:|:    || :  ||
Db          8 TFQKIYHQFLKSTNKEWAKCAPTNVCSP 35
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Search completed: January 5, 2005, 09:15:07
Job time : 548.136 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 33.8182 Seconds
(without alignments)
88.199 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	100.0	185	2	JN0684	adrenomedullin pre
2	157	96.3	188	2	S41600	adrenomedullin - p
3	148	90.8	185	2	JN0766	adrenomedullin pre
4	58.5	35.9	189	2	A85489	hypothetical prote
5	58.5	35.9	189	2	A99638	hypothetical prote
6	58	35.6	430	2	T14536	S-locus-specific g
7	56	34.4	431	2	T14415	S-locus-specific g
8	54	33.1	373	2	G84107	lipopolysaccharide
9	53	32.5	465	2	T15540	hypothetical prote
10	52	31.9	428	2	T14529	S-locus-specific g
11	51	31.3	428	2	T07814	S-locus-specific g
12	51	31.3	429	2	T14533	S-locus-specific g
13	51	31.3	436	2	A27827	S-locus-specific g
14	51	31.3	857	2	T14471	probable S-recepto
15	50	30.7	90	2	C86279	hypothetical prote
16	50	30.7	427	2	T14424	S-locus-specific g
17	50	30.7	428	2	T14423	S-locus-specific g
18	49	30.1	428	2	T14416	S-locus-specific g
19	49	30.1	428	2	T14530	S-locus-specific g
20	49	30.1	429	2	T14528	S-locus-specific g
21	49	30.1	429	2	T07809	S-receptor kinase
22	49	30.1	431	2	T14418	S-locus-specific g
23	49	30.1	431	2	T07812	S-locus-specific g
24	49	30.1	434	2	S04906	S-locus-specific g
25	48.5	29.8	322	2	T47067	hypothetical prote
26	48	29.4	328	2	AG0363	probable cell divi
27	48	29.4	416	2	JC1343	glycylpeptide N-te
28	48	29.4	426	2	T07810	S-locus-specific g
29	48	29.4	444	1	E69130	histidine-tRNA lig
30	48	29.4	689	2	S39531	excinuclease ABC c
31	48	29.4	856	1	JC2482	S-receptor kinase
32	48	29.4	858	1	JC2481	S-receptor kinase
33	48	29.4	1705	2	F71414	hypothetical prote
34	47.5	29.1	438	2	A55070	DNA primase (EC 2.
35	47	28.8	429	2	T14524	S-locus-specific g
36	47	28.8	545	2	A84938	flagellar M-ring p
37	47	28.8	549	2	T33517	hypothetical prote
38	47	28.8	850	2	T14472	S-receptor kinase
39	47	28.8	858	1	JQ1677	S-receptor kinase
40	47	28.8	1004	2	S51133	transposase Tn4652
41	47	28.8	1268	2	A44125	high density lipop
42	47	28.8	1541	1	S71839	canalicular multid
43	46.5	28.5	340	2	S41752	UDP-3-O-[3-hydroxy
44	46	28.2	186	2	H90448	hypothetical prote
45	46	28.2	204	2	AD2607	conserved hypothet

ALIGNMENTS

RESULT 1
JN0684
adrenomedullin precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, T.
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Title: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869; PMID:8074714
A;Accession: JC2351
A;Molecule type: DNA
A;Residues: 1-185 <ISH>
A;Cross-references: UNIPROT:P35318; GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A;Experimental source: pheochromocytoma
R;Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A;Title: Cloning and characterization of cDNA encoding a precursor for human adrenomedu
A;Reference number: JN0684; MUID:93343928; PMID:7688224
A;Accession: JN0684
A;Molecule type: mRNA
A;Residues: 1-185 <KIT>
A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A;Accession: PN0548
A;Molecule type: protein
A;Residues: 22-41 <KI2>
R;Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A;Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocyto
A;Reference number: JN0476; MUID:93249425; PMID:8387282
A;Accession: JN0476
A;Molecule type: protein
A;Residues: 95-146 <KI3>
A;Experimental source: pheochromocytoma
C;Genetics:
A;Gene: GDB:ADM
A;Cross-references: GDB:217070; OMIM:103275
A;Map position: 11pter-11qter
A;Introns: 33/2; 83/2
C;Keywords: amidated carboxyl end; blood pressure control; hormone
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;95-146/Product: adrenomedullin #status experimental <MAT>
F;147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
F;110-115/Disulfide bonds: #status experimental
F;146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following g

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 2
S41600
adrenomedullin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41600
R;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A;Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encc
A;Reference number: S41600; MUID:94139945; PMID:8043068
A;Accession: S41600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-188 <KIT>
A;Cross-references: UNIPROT:P53366; GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

  Query Match             96.3%;  Score 157;  DB 2;  Length 188;
  Best Local Similarity   96.8%;  Pred. No. 2e-15;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||| ||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 3
JN0766
adrenomedullin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JN0766; PN0610
R;Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A;Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A;Reference number: JN0766; MUID:93384621; PMID:7690563
A;Accession: JN0766
A;Molecule type: mRNA
A;Residues: 1-185 <SAK>
A;Cross-references: UNIPROT:P43145
A;Accession: PN0610
A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
essure control.
C;Keywords: amidated carboxyl end
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-185/Product: proadrenomedullin #status predicted <PEU>
F;22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F;94-143/Product: adrenomedullin #status predicted <MAT>
F;41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

  Query Match             90.8%;  Score 148;  DB 2;  Length 185;
  Best Local Similarity   87.1%;  Pred. No. 4.2e-14;
  Matches   27;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |:|||||||||||||| :|||:|||||||
Db        113 TMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143


RESULT 4
A85489
hypothetical protein Z0078 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85489
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85489
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <STO>
A;Cross-references: UNIPROT:Q8XA03; GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:(
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0078
C;Superfamily: Escherichia coli yabP protein

  Query Match             35.9%;  Score 58.5;  DB 2;  Length 189;
  Best Local Similarity   34.4%;  Pred. No. 0.52;
  Matches   11;  Conservative    9;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          4 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 30
              || | : :| :     || :|:| :: :||:|
Db         95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126


RESULT 5
A99638
hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A99638
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A99638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-189 <HAY>
A;Cross-references: UNIPROT:Q8XA03; GB:BA000007; PIDN:BAB33496.1; PID:g13359529; GSPDB:(
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0073
C;Superfamily: Escherichia coli yabP protein

  Query Match             35.9%;  Score 58.5;  DB 2;  Length 189;
  Best Local Similarity   34.4%;  Pred. No. 0.52;
  Matches   11;  Conservative    9;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          4 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 30
              || | : :| :     || :|:| :: :||:|
Db         95 KLTHWLIKFNELKEYAKDPENMAAKASLSPEG 126


RESULT 6
T14536
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14536
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
echanism.
A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Accession: T14536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-430 <KUS>
A;Cross-references: UNIPROT:O23846; EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
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```
  Query Match             35.6%;  Score 58;  DB 2;  Length 430;
  Best Local Similarity   25.6%;  Pred. No. 1.5;
  Matches   10;  Conservative   12;  Mismatches    7;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              :||:: :| ||: :::          ::  |  :||:||
Db        230 EKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268


RESULT 7
T14415
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14415
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
echanism.
A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Accession: T14415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-431 <KUS>
A;Cross-references: UNIPROT:O23849; EMBL:D85215; NID:g2351161; PIDN:BAA21949.1; PID:g235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

  Query Match             34.4%;  Score 56;  DB 2;  Length 431;
  Best Local Similarity   30.8%;  Pred. No. 3;
  Matches   12;  Conservative    8;  Mismatches    9;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              ||| : :| ||:  :|          ::  | ||| :|:
Db        232 QKLNYMVYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270


RESULT 8
G84107
lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G84107
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G84107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <STO>
A;Cross-references: UNIPROT:Q9K6R4; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB073
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3663

  Query Match             33.1%;  Score 54;  DB 2;  Length 373;
  Best Local Similarity   48.0%;  Pred. No. 5;
  Matches   12;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 VQKLAHQIYQFTDKDKDNVAPRSKI 26
              | |||||   ::  |:|:  | ||
Db        132 VYKLAHQIVSLSEGVKENLVRRYKI 156


RESULT 9
T15540
hypothetical protein C17C3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 12-Jul-2004
C;Accession: T15540
R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C17C3.
A;Reference number: Z18366
A;Accession: T15540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-465 <DUZ>
A;Cross-references: EMBL:U41279; NID:g1086905; PID:g1086919; PIDN:AAB52685.1; GSPDB:GN0
A;Experimental source: strain Bristol N2; clone C17C3
C;Genetics:
A;Gene: CESP:C17C3.1
A;Map position: 2
A;Introns: 124/2; 138/2; 174/2; 223/1; 369/2
C;Superfamily: acyl-CoA thioesterase II (TesB) with DUF545 domain

  Query Match             32.5%;  Score 53;  DB 2;  Length 465;
  Best Local Similarity   40.0%;  Pred. No. 9;
  Matches    8;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 QKLAHQIYQFTDKDKDNVAP 22
              |::||: : ||:  ||: :|
Db        156 QEIAHKFFDFTELKKDSFSP 175


RESULT 10
T14529
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14529
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f clas
echanism.
A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Accession: T14529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
A;Cross-references: UNIPROT:O23839; EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g23
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

  Query Match             31.9%;  Score 52;  DB 2;  Length 428;
  Best Local Similarity   28.2%;  Pred. No. 11;
  Matches   11;  Conservative    8;  Mismatches   10;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              |||:: :| ||:  ::          :   | |:|  ||
Db        229 QKLSYMVYNFTENSEEVAYTFRMTNNSFYSRLKVSSDGY 267


RESULT 11
T07814
S-locus-specific glycoprotein S6 - radish (fragment)
C;Species: Raphanus sativus (radish)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07814
R;Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A;Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related ge
A;Reference number: Z16146; MUID:98311079; PMID:9648745
A;Accession: T07814
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <SAK>
A;Cross-references: UNIPROT:O80351; EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g
C;Genetics:
A;Gene: SLG(S6)
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
```

```
F;32-426/Domain: S-locus-specific glycoprotein homology <SSG>

  Query Match             31.3%;  Score 51;  DB 2;  Length 428;
  Best Local Similarity   28.2%;  Pred. No. 16;
  Matches   11;  Conservative    8;  Mismatches   10;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              |||:: :| ||:  ::          ::  |  ||  ||
Db        229 QKLSYMVYNFTENSEEVAYTFLMTNNSIYSRLTISSSGY 267


RESULT 12
T14533
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14533
R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons o f class
echanism.
A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Accession: T14533
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-429 <KUS>
A;Cross-references: UNIPROT:O23843; EMBL:D85209; NID:g2351149; PIDN:BAA21943.1; PID:g235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein

  Query Match             31.3%;  Score 51;  DB 2;  Length 429;
  Best Local Similarity   32.5%;  Pred. No. 16;
  Matches   13;  Conservative    8;  Mismatches    7;  Indels   12;  Gaps    2;

Qy          3 QKLAHQIYQFTDKDKDNVA----------PRSKISPQGY 31
              |||:: :| ||: | : ||           | :|| :|:
Db        230 QKLSYMVYNFTE-DSEEVAYTFRMTNNSIYSRIQISSEGF 268


RESULT 13
A27827
S-locus-specific glycoprotein S6 precursor - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: A27827
R;Nasrallah, J.B.; Kao, T.H.; Chen, C.H.; Goldberg, M.L.; Nasrallah, M.E.
Nature 326, 617-619, 1987
A;Title: Amino-acid sequence of glycoproteins encoded by three alleles of the S locus of
A;Reference number: A93392
A;Accession: A27827
A;Molecule type: mRNA
A;Residues: 1-436 <NAS>
A;Cross-references: UNIPROT:P07761
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-436/Product: S-locus-specific glycoprotein S6 #status predicted <MAT>
F;40-434/Domain: S-locus-specific glycoprotein homology <SSG>

  Query Match             31.3%;  Score 51;  DB 2;  Length 436;
  Best Local Similarity   25.6%;  Pred. No. 16;
  Matches   10;  Conservative   10;  Mismatches    9;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              |||:: :| ||:  ::          ::  |  :| :||
Db        237 QKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275


RESULT 14
T14471
probable S-receptor kinase (EC 2.7.1.-) srk29 - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14471
R;Kumar, V.; Trick, M.
Plant J. 6, 807-813, 1994
A;Title: Expression of the S-locus receptor kinase multigene family in Brassica oleracea
A;Reference number: Z18108; MUID:95152555; PMID:7849754
A;Accession: T14471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-857 <KUM>
A;Cross-references: UNIPROT:Q39392; EMBL:Z30211; NID:g459244; PIDN:CAA82930.1; PID:g459
A;Experimental source: strain alboglabra; stigma
C;Genetics:
A;Gene: srk29
A;Introns: 438/1; 481/1; 544/3; 615/1; 694/2; 744/3
C;Function:
A;Description: implicated in the self-incompatibility system of Brassica oleracea
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal t
F;41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F;526-813/Domain: protein kinase homology <KIN>

  Query Match             31.3%;  Score 51;  DB 2;  Length 857;
  Best Local Similarity   28.2%;  Pred. No. 35;
  Matches   11;  Conservative    8;  Mismatches   10;  Indels   10;  Gaps    1;

Qy          3 QKLAHQIYQFTDKDKD----------NVAPRSKISPQGY 31
              |||:: :| ||   ::          ::  |  || :||
Db        239 QKLSYMVYNFTQNSEEVVYTFRMTNNSIYSRLTISSEGY 277


RESULT 15
C86279
hypothetical protein F14L17.23 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86279
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86279
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STO>
A;Cross-references: UNIPROT:Q9M9R8; GB:AE005172; NID:g7262688; PIDN:AAF43946.1; GSPDB:G
C;Genetics:
A;Map position: 1

  Query Match             30.7%;  Score 50;  DB 2;  Length 90;
  Best Local Similarity   41.9%;  Pred. No. 4;
  Matches   13;  Conservative    3;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||| :|      ||| :    | || :| ||
Db         12 TVQTIARPFTDETDKIQTVPYPPSKHTPPGY 42


Search completed: January  5, 2005, 08:44:40
Job time : 34.8182 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 08:39:22 ; Search time 178.955 Seconds
(without alignments)
99.671 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	100.0	185	1	ADML_HUMAN	P35318 homo sapien
2	163	100.0	185	2	AAP35548	Aap35548 homo sapi
3	157	96.3	188	1	ADML_PIG	P53366 sus scrofa
4	152	93.3	188	1	ADML_CANFA	O77559 canis famil
5	148	90.8	185	1	ADML_RAT	P43145 rattus norv
6	148	90.8	185	2	AAH61775	Aah61775 rattus no
7	146	89.6	188	1	ADML_BOVIN	O62827 bos taurus
8	146	89.6	188	2	Q95KP0	Q95kp0 bos taurus
9	140	85.9	184	1	ADML_MOUSE	P97297 mus musculu
10	140	85.9	184	2	AAH52665	Aah52665 mus muscu
11	138	84.7	27	2	Q9TRZ6	Q9trz6 sus scrofa
12	70	42.9	174	2	Q75XW8	Q75xw8 fugu rubrip
13	70	42.9	174	2	BAD02341	Bad02341 fugu rubr
14	66	40.5	171	2	Q618K5	Q618k5 cyprinus ca
15	66	40.5	171	2	BAD19046	Bad19046 cyprinus
16	58.5	35.9	189	2	Q7AHR7	Q7ahr7 escherichia
17	58.5	35.9	189	2	Q8XA03	Q8xa03 escherichia
18	58	35.6	430	2	O23846	O23846 brassica ol
19	56	34.4	367	2	Q9SEB5	Q9seb5 hirschfeldi
20	56	34.4	425	2	Q84KW0	Q84kw0 brassica ol
21	56	34.4	431	2	O23849	O23849 brassica ca
22	55	33.7	368	2	Q9SBP2	Q9sbp2 raphanus ra
23	55	33.7	421	2	Q8S9B2	Q8s9b2 brassica ol
24	55	33.7	436	2	Q84KX4	Q84kx4 brassica ol
25	55	33.7	438	2	Q84KZ0	Q84kz0 brassica ca
26	54	33.1	373	2	Q9K6R4	Q9k6r4 bacillus ha
27	53.5	32.8	168	2	Q75XW7	Q75xw7 fugu rubrip
28	53.5	32.8	168	2	BAD02342	Bad02342 fugu rubr
29	53.5	32.8	557	2	Q74JC1	Q74jc1 lactobacill
30	53.5	32.8	557	2	AAS09009	Aas09009 lactobaci
31	53	32.5	346	2	Q9BIA5	Q9bia5 caenorhabdi
32	53	32.5	357	2	Q9BIA9	Q9bia9 caenorhabdi
33	53	32.5	431	2	Q84KU5	Q84ku5 brassica ol
34	53	32.5	440	2	Q84KW1	Q84kw1 brassica ol
35	52.5	32.2	159	2	Q75XW6	Q75xw6 fugu rubrip
36	52.5	32.2	159	2	BAD02343	Bad02343 fugu rubr
37	52.5	32.2	269	2	Q6MC13	Q6mc13 parachlamyd
38	52.5	32.2	269	2	CAF23886	Caf23886 parachlam
39	52	31.9	294	2	Q6SV92	Q6sv92 brassica na
40	52	31.9	294	2	Q6SV94	Q6sv94 brassica na
41	52	31.9	294	2	Q6SV96	Q6sv96 brassica na
42	52	31.9	294	2	Q6SVA0	Q6sva0 brassica ca
43	52	31.9	294	2	Q6SVA2	Q6sva2 brassica ca
44	52	31.9	294	2	AAR09046	Aar09046 brassica
45	52	31.9	294	2	AAR09048	Aar09048 brassica

ALIGNMENTS

RESULT 1
ADML_HUMAN
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN Name=ADM; Synonyms=AM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pheochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;
RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT "Cloning and characterization of cDNA encoding a precursor for human
RT adrenomedullin.";
RL Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94354869; PubMed=8074714;
RA Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,
RA Kitamura K., Eto T., Matsuo H.;
RT "Genomic structure of human adrenomedullin gene.";
RL Biochem. Biophys. Res. Commun. 203:631-639(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
RN   [4]
RP   SEQUENCE OF 95-146.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=93249425; PubMed=8387282;
RA   Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
RA   Matsuo H., Eto T.;
RT   "Adrenomedullin: a novel hypotensive peptide isolated from human
RT   pheochromocytoma.";
RL   Biochem. Biophys. Res. Commun. 192:553-560(1993).
RN   [5]
RP   REVIEW.
RX   MEDLINE=98240137; PubMed=9578982;
RA   Samson W.K.;
RT   "Proadrenomedullin-derived peptides.";
RL   Front. Neuroendocrinol. 19:100-127(1998).
RN   [6]
RP   REVIEW.
RX   MEDLINE=20053666; PubMed=10588445;
RA   Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
RT   "Structure-activity relationships of adrenomedullin in the circulation
RT   and adrenal gland.";
RL   Regul. Pept. 85:1-8(1999).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents. Numerous actions have been reported most related to the
CC       physiologic control of fluid and electrolyte homeostasis. In the
CC       kidney, am is diuretic and natriuretic, and both am and pamp
CC       inhibit aldosterone secretion by direct adrenal actions. In
CC       pituitary gland, both peptides at physiologically relevant doses
CC       inhibit basal ACTH secretion. Both peptides appear to act in brain
CC       and pituitary gland to facilitate the loss of plasma volume,
CC       actions which complement their hypotensive effects in blood
CC       vessels.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highest levels found in pheochromocytoma and
CC       adrenal medulla. Also found in lung, ventricle and kidney tissues.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14874; BAA03589.1; -.
DR   EMBL; S73906; AAC60642.1; -.
DR   EMBL; BC015961; AAH15961.1; -.
DR   EMBL; D43639; BAA07756.1; ALT_SEQ.
DR   PIR; JC2351; JN0684.
DR   Genew; HGNC:259; ADM.
DR   MIM; 103275; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0006171; P:cAMP biosynthesis; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0008015; P:circulation; TAS.
DR   GO; GO:0007565; P:pregnancy; TAS.
DR   GO; GO:0006701; P:progesterone biosynthesis; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Polymorphism; Signal.
FT   SIGNAL       1     21
FT   PEPTIDE     22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP      45     92
FT   PEPTIDE     95    146       Adrenomedullin.
FT   PROPEP     148    185       PreproAM C-terminal fragment.
FT   DISULFID    110    115
FT   MOD_RES      41     41       Arginine amide (G-42 provides amide
FT                                group).
FT   MOD_RES     146    146       Tyrosine amide (G-147 provides amide
FT                                group).
FT   VARIANT      50     50       S -> R (in dbSNP:5005).
FT                                /FTId=VAR_014861.
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

  Query Match             100.0%;  Score 163;  DB 1;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-15;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 2
AAP35548
ID   AAP35548    PRELIMINARY;      PRT;   185 AA.
AC   AAP35548;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BT006902; AAP35548.1; -.
SQ   SEQUENCE   185 AA;  20420 MW;  64C7D2A0B4654DFE CRC64;

  Query Match             100.0%;  Score 163;  DB 2;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-15;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||||||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146


RESULT 3
ADML_PIG
ID   ADML_PIG       STANDARD;      PRT;   188 AA.
AC   P53366;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM; Synonyms=AM;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94139945; PubMed=8043068;
RA   Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
RT   "Complete amino acid sequence of porcine adrenomedullin and cloning of
RT   cDNA encoding its precursor.";
RL   FEBS Lett. 338:306-310(1994).
RN   [2]
RP   SEQUENCE OF 22-41.
```

```
RC   TISSUE=Adrenal medulla;
RX   MEDLINE=94357274; PubMed=8076689;
RA   Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,
RA   Kawamoto M., Minamino N., Matsuo H., Eto T.;
RT   "Identification and hypotensive activity of proadrenomedullin N-
RT   terminal 20 peptide (PAMP).";
RL   FEBS Lett. 351:35-37(1994).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adrenal glands, lung and
CC       kidney.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14875; BAA03590.1; -.
DR   PIR; S41600; S41600.
DR   InterPro; IPR001710; Adrenomedullin.
DR   InterPro; IPR011038; Calycin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Hormone; Signal.
FT   SIGNAL        1     21
FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92
FT   PEPTIDE      95    146       Adrenomedullin.
FT   PROPEP      153    188       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID     110    115      By similarity.
FT   MOD_RES       41     41      Arginine amide (G-42 provides amide
FT                                group).
FT   MOD_RES      146    146      Tyrosine amide (G-147 provides amide
FT                                group).
SQ   SEQUENCE   188 AA;  20893 MW;  71749460F5660A61 CRC64;

  Query Match             96.3%;  Score 157;  DB 1;  Length 188;
  Best Local Similarity   96.8%;  Pred. No. 3.8e-14;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||||||| ||||||||||||
Db        116 TVQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146


RESULT 4
ADML_CANFA
ID   ADML_CANFA     STANDARD;      PRT;   188 AA.
AC   O77559; Q9TVC9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Imoto I., Jougasaki M.;
RT   "Cloning of cDNA encoding canine adrenomedullin.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99002704; PubMed=9788655;
RA   Ono Y., Kojima M., Okada K., Kangawa K.;
RT   "cDNA cloning of canine adrenomedullin and its gene expression in the
RT   heart and blood vessels in endotoxin shock.";
RL   Shock 10:243-247(1998).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF045773; AAD05423.1; -.
DR   EMBL; U96127; AAD09957.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92       By similarity.
FT   PEPTIDE      95    146       Adrenomedullin.
FT   PROPEP      148    188       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID     110    115      By similarity.
FT   MOD_RES       41     41      Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES      146    146      Tyrosine amide (G-147 provides amide
FT                                group) (By similarity).
FT   CONFLICT     130    130      N -> K (in Ref. 2).
SQ   SEQUENCE   188 AA;  20929 MW;  809D6A64F98F5578 CRC64;

  Query Match             93.3%;  Score 152;  DB 1;  Length 188;
  Best Local Similarity   93.5%;  Pred. No. 2e-13;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||| ||| ||||||||||||
Db        116 TVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146


RESULT 5
ADML_RAT
ID   ADML_RAT       STANDARD;      PRT;   185 AA.
AC   P43145;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=Adm;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX   MEDLINE=93384621; PubMed=7690563;
RA   Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA   Matsuo H., Eto T.;
RT   "Molecular cloning and biological activities of rat adrenomedullin, a
RT   hypotensive peptide.";
RL   Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
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RX   MEDLINE=96102137; PubMed=8524787;
RA   Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RA   Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RT   "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RT   its role in exacerbating focal brain ischemic damage.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed in adrenal glands, lung, kidney,
CC       heart, spleen, duodenum and submandibular glands.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D15069; BAA03665.1; -.
DR   EMBL; U15419; AAB60519.1; -.
DR   PIR; JN0766; JN0766.
DR   RGD; 2047; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE       22    41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP        45    91       By similarity.
FT   PEPTIDE       94    143      Adrenomedullin.
FT   PROPEP        149   185      PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID      107   112      By similarity.
FT   MOD_RES       41    41       Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES       143   143      Tyrosine amide (G-144 provides amide
FT                                group) (By similarity).
SQ   SEQUENCE   185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;

  Query Match             90.8%;  Score 148;  DB 1;  Length 185;
  Best Local Similarity   87.1%;  Pred. No. 7.2e-13;
  Matches   27;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |:|||||||||||||||| :|||:|||||||
Db        113 TMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143


RESULT 6
AAH61775
ID   AAH61775    PRELIMINARY;      PRT;   185 AA.
AC   AAH61775;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC061775; AAH61775.1; -.
SQ   SEQUENCE   185 AA;  20636 MW;  35CAD9A9DD19AE35 CRC64;

  Query Match             90.8%;  Score 148;  DB 2;  Length 185;
  Best Local Similarity   87.1%;  Pred. No. 7.2e-13;
  Matches   27;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |:|||||||||||||||| :|||:|||||||
Db        113 TMQKLAHQIYQFTDKDKDGMAPRNKISPQGY 143


RESULT 7
ADML_BOVIN
ID   ADML_BOVIN     STANDARD;      PRT;   188 AA.
AC   O62827;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=ADM;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RX   MEDLINE=98244567; PubMed=9585168;
RA   Barker S., Wood E., Clark A.J.L., Corder R.;
RT   "Cloning of bovine preproadrenomedullin and inhibition of its basal
RT   expression in vascular endothelial cells by staurosporine.";
RL   Life Sci. 62:1407-1415(1998).
CC   -!- FUNCTION: Hypotensive peptide. May function as a hormone in
CC       circulation control (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001613; CAA04866.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
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FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92       By similarity.
FT   PEPTIDE      95    146       Adrenomedullin.
FT   PROPEP      148    188       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID    110    115       By similarity.
FT   MOD_RES      41     41       Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES     146    146       Tyrosine amide (G-147 provides amide
FT                                group) (By similarity).
SQ   SEQUENCE   188 AA;  20981 MW;  3002E79AB3B6612C CRC64;

  Query Match             89.6%;  Score 146;  DB 1;  Length 188;
  Best Local Similarity   90.3%;  Pred. No. 1.4e-12;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||| |||||||  ||||||||||
Db        116 TVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146


RESULT 8
Q95KP0
ID   Q95KP0      PRELIMINARY;      PRT;   188 AA.
AC   Q95KP0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Adrenomedullin.
GN   Name=pBAM-2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21630318; PubMed=11754956;
RA   Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RA   Kangawa K., Eto T.;
RT   "Adrenomedullin (11-26): a novel endogenous hypertensive peptide
RT   isolated from bovine adrenal medulla.";
RL   Peptides 22:1713-1718(2001).
DR   EMBL; AB055107; BAB62176.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
SQ   SEQUENCE   188 AA;  20963 MW;  6102E69A756DCA86 CRC64;

  Query Match             89.6%;  Score 146;  DB 2;  Length 188;
  Best Local Similarity   90.3%;  Pred. No. 1.4e-12;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||| |||||||  ||||||||||
Db        116 TVQKLAHQIYHFTDKDKDGSAPRSKISPQGY 146


RESULT 9
ADML_MOUSE
ID   ADML_MOUSE     STANDARD;      PRT;   184 AA.
AC   P97297; P97453;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE   terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
GN   Name=Adm;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=97092892; PubMed=8938454;
RA   Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
RA   Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
RT   "Genomic organization, expression, and chromosomal mapping of the
RT   mouse adrenomedullin gene.";
RL   Genomics 37:395-399(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99046755; PubMed=9808778;
RA   Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
RA   Ko M.S.H.;
RT   "Expression of adrenomedullin, a hypotensive peptide, in the
RT   trophoblast giant cells at the embryo implantation site in mouse.";
RL   Dev. Biol. 203:264-275(1998).
CC   -!- FUNCTION: AM and PAMP are potent hypotensive and vasodilatator
CC       agents.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the adrenomedullin family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D78349; BAA11367.1; -.
DR   EMBL; U77630; AAB36535.1; -.
DR   MGD; MGI:108058; Adm.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT   SIGNAL        1     21       By similarity.
FT   PEPTIDE      22     41       Proadrenomedullin N-20 terminal peptide.
FT   PROPEP       45     92       By similarity.
FT   PEPTIDE      95    144       Adrenomedullin.
FT   PROPEP      151    184       PreproAM C-terminal fragment (By
FT                                similarity).
FT   DISULFID    108    113       By similarity.
FT   MOD_RES      41     41       Arginine amide (G-42 provides amide
FT                                group) (By similarity).
FT   MOD_RES     144    144       Tyrosine amide (G-145 provides amide
FT                                group) (By similarity).
FT   CONFLICT    173    173       A -> G (in Ref. 2).
SQ   SEQUENCE   184 AA;  20764 MW;  C88C99045A79C898 CRC64;

  Query Match             85.9%;  Score 140;  DB 1;  Length 184;
  Best Local Similarity   83.9%;  Pred. No. 1e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              | |||||||||| |||||| :|||:|||||||
Db        114 TFQKLAHQIYQLTDKDKDGMAPRNKISPQGY 144


RESULT 10
AAH52665
ID   AAH52665    PRELIMINARY;      PRT;   184 AA.
AC   AAH52665;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Egg;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Egg;
RA   Strausberg R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC052665; AAH52665.1; -.
SQ   SEQUENCE   184 AA;  20750 MW;  C88C9903C479C898 CRC64;

  Query Match             85.9%;  Score 140;  DB 2;  Length 184;
  Best Local Similarity   83.9%;  Pred. No. 1e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              | ||||||||| |||||| :|||:|||||||
Db        114 TFQKLAHQIYQLTDKDKDGMAPRNKISPQGY 144


RESULT 11
Q9TRZ6
ID   Q9TRZ6      PRELIMINARY;      PRT;    27 AA.
AC   Q9TRZ6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   ADRENOMEDULLIN.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96157714; PubMed=8576091;
RA   Ichiki Y., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.;
RT   "Distribution and characterization of immunoreactive adrenomedullin in
RT   porcine tissue, and isolation of adrenomedullin [26-52] and
RT   adrenomedullin [34-52] from porcine duodenum.";
RL   J. Biochem. 118:765-770(1995).
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
SQ   SEQUENCE   27 AA;  3063 MW;  B8DC7FA18D8B3D90 CRC64;

  Query Match             84.7%;  Score 138;  DB 2;  Length 27;
  Best Local Similarity   96.3%;  Pred. No. 2.3e-12;
  Matches   26;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 LAHQIYQFTDKDKDNVAPRSKISPQGY 31
              |||||||||||||| ||||||||||||
Db          1 LAHQIYQFTDKDKDGVAPRSKISPQGY 27


RESULT 12
Q75XW8
ID   Q75XW8      PRELIMINARY;      PRT;   174 AA.
AC   Q75XW8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-1.
GN   Name=ADM1;
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120295; BAD02341.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
SQ   SEQUENCE   174 AA;  20222 MW;  61535E41FCF88D4D CRC64;

  Query Match             42.9%;  Score 70;  DB 2;  Length 174;
  Best Local Similarity   48.4%;  Pred. No. 0.094;
  Matches   15;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||  || :::|   : | ::||  |||||||
Db        102 TVHDLAFRLHQLGFQYKIDIAPVDKISPQGY 132


RESULT 13
BAD02341
ID   BAD02341    PRELIMINARY;      PRT;   174 AA.
AC   BAD02341;
DT   14-APR-2004 (TrEMBLrel. 27, Created)
DT   14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT   14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adrenomedullin-1.
GN   ADM1.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22984567; PubMed=14623291;
RA   Ogoshi M., Inoue K., Takei Y.;
RT   "Identification of a novel adrenomedullin gene family in teleost
RT   fish.";
RL   Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR   EMBL; AB120295; BAD02341.1; -.
SQ   SEQUENCE   174 AA;  20222 MW;  61535E41FCF88D4D CRC64;

  Query Match             42.9%;  Score 70;  DB 2;  Length 174;
  Best Local Similarity   48.4%;  Pred. No. 0.094;
  Matches   15;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||  || :::|   : | ::||  |||||||
Db        102 TVHDLAFRLHQLGFQYKIDIAPVDKISPQGY 132
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RESULT 14
Q6L8K5
ID   Q6L8K5      PRELIMINARY;      PRT;   171 AA.
AC   Q6L8K5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Preproadrenomedullin precursor.
GN   Name=preproAM;
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   PubMed=15242754;
RA   Kono T., Sakai M.;
RT   "Molecular cloning and expression of preproadrenomedullin gene from
RT   common carp Cyprinus carpio L.";
RL   Gen. Comp. Endocrinol. 138:78-88(2004).
DR   EMBL; AB120940; BAD19046.1; -.
DR   InterPro; IPR001710; Adrenomedullin.
DR   Pfam; PF02039; Adrenomedullin; 1.
DR   PRINTS; PR00801; ADRENOMEDULN.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        79    127       adrenomedullin.
SQ   SEQUENCE   171 AA;  19412 MW;  A9595B9A11E5AC36 CRC64;

  Query Match             40.5%;  Score 66;  DB 2;  Length 171;
  Best Local Similarity   45.2%;  Pred. No. 0.34;
  Matches   14;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||  |||:::   :| |   ||  ||:| ||
Db         97 TVHVLAHRLHDLNNKLKIGNAPADKINPFGY 127


RESULT 15
BAD19046
ID   BAD19046    PRELIMINARY;      PRT;   171 AA.
AC   BAD19046;
DT   20-MAY-2004 (TrEMBLrel. 27, Created)
DT   20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT   20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE   Preproadrenomedullin precursor.
GN   PREPROAM.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Kono T., Sakai M.;
RT   "Molecular cloning of a novel preproadrenomedullin gene from common
RT   carp Cyprinus carpio L. and its expression.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB120940; BAD19046.1; -.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        79    127       adrenomedullin.
SQ   SEQUENCE   171 AA;  19412 MW;  A9595B9A11E5AC36 CRC64;

  Query Match             40.5%;  Score 66;  DB 2;  Length 171;
  Best Local Similarity   45.2%;  Pred. No. 0.34;
  Matches   14;  Conservative    5;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
              ||  |||:::   :| |   ||  ||:| ||
Db         97 TVHVLAHRLHDLNNKLKIGNAPADKINPFGY 127


Search completed: January  5, 2005, 08:43:47
Job time : 179.955 secs
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